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                                                                     Sequence 1, A Sequence 11, B Sequence 1, B Sequence 5, A Sequence 25, B Sequence 25, B Sequence 29, B Sequence 1, A Sequence 5, A Sequence 1, A Sequence 5, A Sequence 5, A Sequence 1, A Sequence 5, 
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Sequence 13
    Sequence Sequence S
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APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
US-08-318-826A-5
US-08-370-156-1
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NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-146-283-3
; Sequence 3, Application US/09146283
; Patent No. 5976546
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LENGTH: 2385 base pairs
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ADDRESSEE: Dehlinger
  USA
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COUNTRY: (
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MODEL-frame+p20.model -DEV-xlp
-Q-/cgn2_L/VBPTO_SPOOL_p/HOLLERAN480/runat_15102003_131913_20570/app_query fasta_1.4685
-Q-/cgn2_L/VBPTO_SPOOL_p/HOLLERAN480/runat_15102003_131913_20570/app_query fasta_1.4685
-DB=ISSUEd_Zatents_NA -OFWH=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXTT 0 -UNITS=bits -STRAT=1 -END=-1 -NATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR_SCORE=pct -TRR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                                                       October 15, 2003, 22:55:19; Search time 7.60488 Seconds (without alignments) 1741.185 Million cell updates/sec
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

    nucleic search, using frame_plus_p2n model

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1 DKGCPAEQRASPLTSQNEDLGPSSPMDSTF 30
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US-08-229-515A-14
US-08-645-865-14
US-09-048-804-1
US-09-056-105-26
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US-09-344-195-3
US-08-776-251-3
US-08-776-251-10
US-08-625-101-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-146-283-3
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Perfect score:
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1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeu 20
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INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24 Jun-1999
CLASSIFICATION: <u >Unknown></u>
 INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruegg, Curtis L.
Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-579-823A-3 (1-2385)
                                                                                                                     Conservative:
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APPLICATION UNBER: US/09/146,283
APPLICATION UNBER: 03-SEPT-1998
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7536-0010.21
                                                                                                                                       Mismatches:
Indels:
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STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
                                                                                                 Matches:
                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                     1985 CGCTCGCCCAGCCCC 1999
                                                                                                                                                                                                                                                                                                                                 21 GlyProSerSerPro 25
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                               82.00
68.00%
68.00%
51.25%
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                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                             Alignment Scores:
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                 ÚS-08-579-823A-3
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Patent No. 6080409
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Rueggy Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                       ) ORGANISM: homo sapiens
) INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig.
US-09-146-283-3
                                                                                                                                                                                                                                                                                                                                                                     JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-146-283-3 (1-2385)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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STREET: 350 Cambridge Ave. Suite 250
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ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFRENCE/DOCKET NUMBER: 7636
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0960
                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapiens
TYPE: nucleic acid
STRANDEDNESS: double
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EDNESS: double
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Best Local Similarity:
Query Match:
                                                                                                                 ORIGINAL SOURCE:
ORGANISM: home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                 ANTI - SENSE: NO
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US-08-776-251-10

Sequence 10, Application US/08776251

Sequence 10, Application US/08776251

Patent No. 6025340

GENERAL INFORMATION:
APPLICANT: Springer, Caroline J
APPLICANT: Marais, Richard
TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug thera
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
                                Sequence 3, Application US/09200355
Patent No. 6451524
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
FILE REFERENCE: IBISO009
CURRENT APPLICATION UNMBER: US/09/200,355
CURRENT FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,251
FILING DATE: 31-Jah-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   201
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STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
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Mismatches:
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Matches:
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FILING DATE: 27-JUL-1995
PRIOR APPLICATION DATE: 37-JUL-1995
APPLICATION NUMBER: GB 9415167.7
FILING DATE: 27-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620-20
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       0.000424
                                                                                                                                                                                                                                                                                                                                                                                          80.00
100.00%
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50.00%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens US-09-200-355-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA US-08-776-251-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 201
                    US-09-200-355-3
                                                                                                                                                                                                                                                                          TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Springer, Caroline J
APPLICANT: Springer, Caroline J
APPLICANT: Marais, Richard
TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     MEDICATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/776,251
FILING DATE: 31-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01782
FILING DATE: 27-JUL-1995
RIOR APPLICATION NUMBER: GB 9415167.7
FILING DATE: 27-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6025340th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                   JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-344-195-3 (1-2385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-776-251-3 (1-153)
                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
Length:
Matches:
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Matches:
                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08776251
Patent No. 6025340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           1985 CGCTCGCCCAGCCCC 1999
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80.00
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50.00%
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                    82.00
68.00%
68.00%
51.25%
0.00524
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA US-08-776-251-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                  Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                   US-08-776-251-3
                                                                            Query Match:
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  Pred. No.:
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1915 GACAAGGGCTGCCCCGCCGAGCAGAGACCCAGCCCTCTGACGTCC 1959
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.3768
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                       02109
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                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cheever, Martin A.
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                         1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3768
15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-625-101-1 (1-3768)
                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TENGTH: 3768 base pairs
TENGTH: and acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08625101
Patent No. 5869445
GENERAL INFORMATION:
                                0.00262
80.00
100.00%
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50.00%
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100.00%
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98104-7092
                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                    US-08-625-101-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-625-101-1
                                                                                                              Query Match:
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                                                                                                                                                                                                                                                                                        RESULT 7
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APPLICANT: Huston, James S.
APPLICANT: Huston, James S.
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
APPLICANT: Houston, L. L.
TAPLE OF INVENTION: Biosynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-356-786-1 (1-3768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "product = "cerB-b2""
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PItcher, Edmund R.
REFERENCE/DOCKET NUMBER: CRP-053
FEFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-229-515A-14; Sequence 14, Application US/08229515A; Patent No. 5518885; GENERAL INFORMATION:
Sequence 1, Application US/08356786
Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
100.00%
50.00%
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Alignment Scores:
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TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: BEBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-229-515A-14 (1-3955)
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                            NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/229,515A FILING DATE: 19 APR 1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1414.608
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                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414
FELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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100.00%
50.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3955 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Atlanta
STATE: Georgia
COUNTRY: usa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-645-865-14
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia
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Patent No. 5968748
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
TITLE OF INVENTION: AWTISENSE OLIGONUCLEOTIDE MODULATION OF
TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE S. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-645-865-14 (1-3955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER TEADABLE FORM:
MEDIUM TYPE: 1.44 Mb diskette
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/048,804
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
RECISTRATION NUMBER: 33.438
REFERENCE/DOCKET NUMBER: 1144.608
TELECOMONICATION INFORMATION:
TELECHOME: 404-688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION UNDRER: 38,534
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               TELEFAX: 404-688-9890
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
14 MAY 1996
                                                                                                                                                                                                                                                                                                                                                              0.0205
80.00
100.00%
100.00%
50.00%
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TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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US-08-645-865-14
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APPLICANT: KIPPS, THOMAS J.
APPLICANT: WIN YUNGI
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT PELLOR DATE: 1998-04-06
CURRENT PELLOR DATE: 1998-04-06
EARLIER APPLICATION NOWBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF EQUID NOS: 35
SOFTWARE: FastERQ for Windows Version 3.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SARKAR, FAZUUL H
APPLICANT: SARKAR, FAZUUL H
TITLE OF INVENTION: BRBB1 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUNC_SEQ3_SEQ2RES991_ (1-30) x US-09-056-105-26 (1-4473)
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                  Conservative:
Mismatches:
Indels:
 Length:
Matches:
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Matches:
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                                                                                                                                                                                                                                                             Sequence 26, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
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0.024
80.00
100.00%
100.00%
50.00%
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100.00%
100.00%
50.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: usa
ZIP: 30303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4473
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                                                                      Query Match:
 Pred. No.:
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APPLICANT: SARKAR, FAZLUL H
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-229-515A-9 (1-4530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                  Matches:
                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEPHONE: 404-688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08645865
patent No. 5654406
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORREY-AGENT INFORMATION:
NAME: PEREYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFRENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
                                                                                                                                          INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 4530 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                              80.00
100.00%
100.00%
50.00%
FILING DATE: 19 APR 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4530 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: "FT
                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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US-08-229-515A-9
                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
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US-08-645-865-9
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Alignment Scores:

Search completed: October 16, 2003, 17:16:03 Job time : 18.6049 secs

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APPLICANT Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
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COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: BLOPPY disk
COMPUTER: DEPERT FORDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION OWNER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
   4530
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                                                                                                                                                                                                                                                       JUNC_SEQ3_SEQ2RES991_ (1-30) x US-08-645-865-9 (1-4530)
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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APPLICATION NUMBER: PCI/US97/00582
FILING DATE: AURANOM***
ATORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 7933-33 PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09167322; Patent No. 6365151; GENERAL INFORMATION:
                                         80.00
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                                                                   Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
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                                                                                                                                                  Query Match:
   Pred. No.:
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Title: Perfect score: Sequence:

Scoring table:

Searched:

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Sequence 3, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 24, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 37, Appli
Sequence 174, Appli
Sequence 175, Appli
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPONDS FOR ELLCITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
4 US-09-676-610B-17

1 US-08-464-41B-3

2 US-08-237-401A-3

3 US-09-632-580A-3

3 US-09-632-580A-3

1 US-08-464-438-1

3 US-09-103-840A-1

9 US-09-103-840A-1

4 US-09-103-840A-1

9 US-09-670-314-4

4 US-09-670-314-4

4 US-09-670-318-1

4 US-09-410-551B-30

4 US-09-410-551B-30

4 US-09-410-551B-31

4 US-09-410-551B-32

4 US-09-410-551B-32

4 US-09-410-551B-32

4 US-09-410-551B-28

4 US-09-410-551B-28

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4 US-09-410-551B-28

4 US-09-410-551B-20

4 US-09-410-551B-20

4 US-09-410-551B-20

4 US-09-410-551B-18

6 US-09-410-551B-18

7 US-08-843-951-1

4 US-09-410-551B-18

8 US-09-410-551B-18

8 US-09-410-551B-18

8 US-08-843-366-23

3 US-08-843-386-23

3 US-08-843-386-23
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NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08625101
Patent No. 5869445
        2532 4 2437 11 24403765 4 411802 9 4 4703765 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737 4 4737
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CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98104-7092
                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-625-101-1
          277
249.5
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244.5
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154.5
153.146.5
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            Sequence 1, Appli
Sequence 26, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 1, Appli
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Sequence 14, Appl
Sequence 14, Appl
Sequence 3, Appli
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                                                                                                                                               October 15, 2003, 22:55:19 ; Search time 67.4299 Seconds (without alignments) 1741.185 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                           .....TFKGTPTAENPEYLGLDVPV 266
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                             OM protein - nucleic search, using frame_plus_p2n model
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US-08-356-786-1
US-09-056-105-26
US-09-056-105-26
US-08-645-865-9
US-09-527-487-1
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US-08-645-865-14
US-08-475-035-3
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Maximum DB seq length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
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266
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Matches:
Conservative:
Mismatches:
Indels:
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1450.00
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   LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS
                                                1..3765
                                                                                                    Best Local Similarity:
                                                                                             Percent Similarity:
                                                                      Alignment Scores: Pred. No.:
                                                  ; LOCATION:
US-08-625-101-1
                                           NAME/KEY:
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                                                                                                                                          APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                          E: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
Exchange Place, 53 State Street
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266
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APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
CLACTORY
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                      Sequence 1, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
3748 GGTCTGGACGTGCCAGTG 3765
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REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
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APPLICATION NUMBER: 07/82
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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OTHER INFORMATION:
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Query Match:
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AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp
                                                              ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TITLE OF INVENTION: HUMAN HER-2 EXPRESSION NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 596874 STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5968748
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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STREET: One Liberty
CITY: Philadelphia
STATE: PA
COUMTRY: U.S.A.
ZIP: 19103
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US-09-048-804-1
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LeuGlyMetGlyAlaAlaLySGlyLeuGlnSerLeuProThrHisAspProSerProLeu
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Mismatches:
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Matches:
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REGISTRATION NUMBER: 38,534
REGERENCE/DOCKET NUMBER: ISIS-2913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4473 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                   SEQ4 (1-266) x US-09-048-804-1 (1-4473)
                                                                                                                                                                                                          1.57e-104
1450.00
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Best Local Similarity:
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STRANDEDNESS:
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ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260
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                                                                                                                                             GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
APPLICANT: KIPPS, THOMAS J.
APPLICANT: WID, YUNDI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR;
TITLE OF INVENTION: PROCESSING;
FILE REFERENCE: 233/221
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
SAGING OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
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266
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Matches:
Conservative:
Mismatches:
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                                                                                                                        Sequence 26, Application US/09056105
Patent No. 6287569
                                                            3922 GGTCTGGACGTGCCAGTG 3939
                                               261 GlyLeuAspValProVal 266
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1450.00
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Best Local Similarity:
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US-09-056-105-26
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3622 CCTTCGCCCCGAGAGGCCCCTCTGCCTGCTGCCGACCTGCTGGTGCCACTCTGGAAAGG
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                                                                                                                                      201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro
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APPLICANT: RAZIUDIN
APPLICANT: RAZIUDIN
APPLICANT: BRAKA, FAZLUL H
TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SUGUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: PERRYAAN, DAVID G
REGISTRATION NUMBER: 33,438
REPERENCE/DOCKET NUMBER: 1414.608
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches:
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Mismatches:
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; Patent No. 5518885
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EDNESS: single
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                                    GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
                             GluAspAspAspMetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly
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APPLICANT: RAZIUDDIN
APPLICANT: SARKAR FAZLUL H
APPLICANT: SARKAR FAZLUL H
APPLICANT: SARKAR FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Aclanta
STATE: Georgia
COUNTRY: usa
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Patent No. 5654406
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                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865 FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTORNEY/AGENT 187
NAME: PERRYMAN, DAVID G
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                     Length:
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                                                                                                                                                                    REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404.688-0770
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ4 (1-266) x US-08-645-865-9 (1-4530)
                                                                                                                                                                                                                                                                                                                                                                                 6.78e-104
1442.00
99.62%
99.62%
                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 30303
COMPUTER READABLE FORM:
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US-08-645-865-9
                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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3118 CAGAATGAGGACTTGGGCCCAGCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTG
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       1 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu
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TITLE OF INVENTION: HERZ ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILING DATE: 2000-03-16
NUMBER OF EDC ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
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Patent No. 6528060
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ORGANISM: Homo sapiens
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                                               AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro
                                                                           GCCGTGGAGAACCCCGAGTACTTGACACCCCAGGGAGGAGCTGCCCCTCAGCCCCACCT
                                                                                                                                               ProProAlaPheSerProAlaPheAspAsnLeuTyrTyrTrpAspGlnAspProProGlu
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STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FLING DATE: 07-Oct-1998
CLASSIFICATION: <a href="Chicago: Chicago: Chica
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MODACO, DADIEL A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciences, Halpern, Michael
England, James M.
TITLE OF INVENTION: CANCER VACCINE
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Patent No. 6365151
GENERAL INFORMATION:
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SEQ ID NO: 4:
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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Pred. No.:
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US-09-167-322-4
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; LOCATION: (151)..(3915)
US-09-527-487-1
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Best Local Similarity:
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US-09-877-177A-11
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APPLICANT: K. Danenberg
TITLE OF INVEWION: Method of determining Epidermal Growth
TITLE OF INVEWION: Factor Receptor and HER2-New Gene Expression
TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
FILE REPERENCE: 11220/120
CURRENT APPLICATION NUMBER: US/09/877,177A
CURRENT APPLICATION NUMBER: 201-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
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cal Similarity:
GENERAL INFORMATION:
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Qy 61 SerSerThrArgSerGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGluGlu 80	Db 3179 TCGTCCACCAGGAGTGGTGGTGGTGGTGACCTGACACTGGGCCTGGAGCCTCGGAAGAGAGGG 323	Qy 81 AlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp 100	3239 CCCCCCAGATCTCCACTGGCTCCCTCGGAAGGGGCTTGCTT	Oy 101 LeuGlyMetGlyAlaAladysGlyLeuGlnSerLeuProThrHisAspProSerProLeu 120	121 GlnArgTyrSerGluAspProThrValProLeuProSerGluThrAspGlyTyrValAla	Db 3359 CAGCGGTACAGCGAGGACCCCCATTACCTCTGCCCCCGAGACTGATGGCTÄTGTTGCT 3418	Qy 141 ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro 160	161 ProSerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArg 1	Db 34/9 CCTTTAACCCCAGAGGTCCTCTGCCTCTGTCCTGCTGGTGCTACTCTAGAAAGA 3538	101 F1019 3111 Deutschift odat y Lysanich y valvahlingsas y valvahling menskriedt y dag valvahling menskriedt y da	201 AlaValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisPro	Db 3599 GCTGTGGAGAACCCTGAATACTTAGTACCGAGAGAAGACGCCCTCTCCGCCCCACCCT 3658	Qy 221 ProProAlaPheSerProAlaPheAspAsnLeuTyrTrpAspGlnAspPtoProGlu 240	241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu	Db 3719 CAGGGCCTCCACCAAGTAACTTTGAAGGGACCCCCACTGCAGAAACCTG 3778	Qy 261 GlyLeuAspValProVal 266	Db 3779 GCCTGGATGTACCTGTA 3796	RESULT 11 US-08-645-865-14 ; Sequence 14, Application US/08645865	; Patent NO. 5654406 ; GENERAL INFORMATION: . ADDITCAMP: DATIFIED	APPLICANT: SARKAR, FAZLUL H ; TITLE OF INVENTION: ERBEZ PROMOTER BINDING PROTEIN IN ; TITLE OF INVENTION: NEOPLASTIC DISEASE	; NUMBER OF SEQUENCES: 19 ; CORRESPONDENCE ADDRESS: 1 ; ADDRESSEE: NEEDLE & ROSENBERG PC	; STREET: 127 Peachtree Street, Suite 1200 ; CITY: Atlanta	; STATE: Georgia ; COUNTRY: usa	COMPUTER READABLE FORM: HEDIUM TYPE: Floppy disk COMPUTED: TAM DO COMMA+ible	COFTWARE: PatentIn Release #1.0, Version #1.30		CLASSIFICATION: 4 TAN 1790 CLASSIFICATION: ATTORNEY/AGENT INFORMATION:
Db 3778 CCTCCTGCCTTCAGCCCAGCCTTCGACAACCTCTATTACTGGGACCAGGACCACCAGGAG 3837	Oy 241 ArgGlyAlaProProSerThrPheLysGlyThrProThrAlaGluAsnProGluTyrLeu 260	Db 3838 CGGGGGGTCCACCCAGCACCTTCAAAGGGACACCTACGGCAGAGAACCCAGAGTACCTG 3897	261 GlyLeuAspValProVal 266	DD 3898 GGICTGGACGIGCCAGIG 3915 RESULT 10	CA CA S	; Falceit No. 5518885 ; GENERAL INFORMATION: ; APPLICANT: RAZIUDDIN		SE EE:) SINDEL: 12/ FEACHLINE SLIEEL, SUITE 1200 ; CITY: Atlanta : STAMTE. Georgia	COUNTRY: usa	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible	<pre>; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30</pre>	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/229,515A ; FILING DATE: 19 APR 1994	; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION:	; NAME: PERRYMAN, DAVID G ; REGISTRATION NUMBER: 33,438 : REFERENCE/DACKER NUMBER: A114 608	ATION:	; TELEFAX: 404-688-9880 ; INFORMATION FOR SEQ ID NO: 14;	🖰	9	ent Scores: 1.31e-85 Length:	larity: 87.59% imilarity: 83.83%	Indels: Gaps:	SEQ4 (1-266) x US-08-229-515A-14 (1-3955)	Oy I GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeuLeu 20	40	Db 3059 GAAGATGACATGACATGGCTGACCTGGAAGAGTATCTGGTGCCCCAGCAGGA 3118	Oy 41 PhePheCysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer 60

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Matches:
Conservative:
Mismatches:
Indels:
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     TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                         1.31e-85
1208.00
87.59%
83.83%
REFERENCE/DOCKET NUMBER:
                                                                                                                                 Percent Similarity:
Best Local Similarity:
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Pred. No.:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,035
FILING DATE: 7 Jun 1995
CLASSIFICATION: 435
ATYONEY/AGFN"
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Matches:
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Mismatches:
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Patent No. 598553
GENERAL INFORMATION:
APPLICANT: KRAUS, MATTHIAS H.
APPLICANT: AARONSON, STUBRT A.
TITLE OF INVENTION: EGF RECEPTOR GENE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.656
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ4 (1-266) x US-08-475-035-3 (1-5532)
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 3:
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277.00
42.75%
31.52%
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TYPE: nucleic acid
STRANDEDNESS: single
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187..3816
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STATE: Georgia
COUNTRY: USA
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Best Local Similarity:
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CITY: At
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US-08-475-035-3
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AspLeuThrLeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaPro
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                                                            SerGluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLySGly
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Patent No. 6444465
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: C. Stank Bennett
APPLICANT: Susan M. Ereier
TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
FILE REFERENCE: RTS-0138
CURRENT APPLICATION NUMBER: US/09/676,610B
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 17
LENGTH: 5532
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277.00
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US-09-676-610B-17
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Patent No. 5811516
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
(1-266) x US-09-676-610B-17 (1-5532)
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US-08-456-647B-3
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1569 CAGAGGTATAGTGCTGATCCCACAGTGTTCGCCCCAGAACGGAATCCTCGAGAGACTG 1628
                                                                   1785 -----GCGGAGGATGAATACGTGAATGAGCCTCTATACCTCAACACCTTCGCCAATGCC 1838
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                                                                                                                               154 ProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAlaArgPro 173
                                                                                                                                                                                                                                                                                                              202 ValGluAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaProGlnProHisProPro 221
                                         134 GluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrValAsnGln
                                                                                                                                                                                                                       174 AlaGlyAlaThrLeuGluArgProLys-----ThrLeuSerProGlyLysAsn
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                                                                                                                                                                           1689 GTGGAAGAGAACCCTTTTGTGTCCCGAAGGAAGAATGGAGATCTTCAAGCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08237401A
Patent No. 5837448
GENERAL INFORMATION:
ADDICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4.225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/POCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Haile Ph.D., Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 2437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-237-401A-3
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87
39
104
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                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GlnArgTyrSerGluAspProThrValProLeuProSer--
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Matches:
Conservative:
Mismatches:
Indels:
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RECISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5090
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 2437 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION WOMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION WOMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
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249.50
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29.49%
17.21%
                  COMPUTER READABLE FORM:
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Best Local Similarity:
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US-08-456-647B-3
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1341 -----ATCTACACATCCAGAACAAGAATTGACTCCAATAGGAATTGTG 1388
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                        1.16e-10
249.50
42.718
29.498
17.218
TOPOLOGY: linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
CLONE: TYPO-2
FEATURE:
                                                                          3..2118
                                                                                                                                      Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                             ; NAME/KEY:
; LOCATION:
US-08-237-401A-3
                                                                                                               Alignment Scores:
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Search completed: October 16, 2003, 17:18:11 Job time : 100.43 secs

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CADUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: END PC compatible
COMPUTER: PLOPPY disk
COMPUTER: PACHOLIAN: PC-DOS/MS-DOS
SOFTWARE: PACHOLIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7536-0010.21
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                              US-08-229-515A-14
US-08-676-610B-17
US-09-676-610B-17
US-09-676-610B-17
US-09-676-610B-17
US-09-676-610B-17
US-08-484-43B-11
US-08-484-43B-11
US-08-473-119-3
US-08-473-119-3
US-09-676-610B-25

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STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09146283
Patent No. 5976546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 2385 base pairs
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    \begin{array}{c} 1.15\, \text{Ke} \\ 1.05\, \text{Ke} \\ 2.05\, \text{C} \\ 3.05\, \text{C
    USA
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COUNTRY: US
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-146-283-3
MODEL-frame+_p2n.model -DEV-xlp

-WODEL-frame+_p2n.model -DEV-xlp

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-LISS=45 - DOCALIGN=200 -THR SCORE=pct - THR_MAX=100 -TRR_MIN=0 - ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
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3628
1 MELAALCRWGLLLALLPPGA......CVDLDDKGCPAEQRASPLTS 653
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2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
                                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-344-195-3
US-09-344-195-3
US-08-625-101-1
US-09-048-804-1
US-09-056-105-26
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Matches:
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                                                ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2
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STRANDENESS: double
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTT-SENSE: NO
ORIGINAL SOURCE.
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                                                                                               GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGTGCCGA
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                                   GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
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Db 1871 GGGGGTGCCGAGCCTTGCCCATGAACTGCACCCACCTGCGTGGACCTGGATGACAAG 1930	Qy 641 GlycysProAlaGluGlnArgAlaSerProLeuThrSer 653	RESULT 2 US-08-579-823A-3 Sequence 3, Application US/08579823A	SENERAL INFORMATION: APPLICANT: Laus, Reiner APPLICANT: Ruegy, Curtis L.	ENTION: Immur QUENCES: 10 CE ADDRESS:	ADDEASEL: Definition of Associates STREET: 350 Cambridge Ave. Suite 250 CITY: Palo Alto STATE: CA COMMENS. 103	306 EAD YPE	SYST Pat LICAT	FILING DATE: 03-DEC-1998 ; CLASSIFICATION: 536 ; ATTORNEY FAGENT INCRMATION:	NAME: JUGGE, LINIGA K. REGISTRATION NUMBER: 42,702 REFERENCE/DOCKET NUMBER: 7636-0010 TELECOMMUNICATION INFORMATION:	I ILEPERAX: 650-324-0960 ; INFORMATION FOR SEQ ID NO: 3: ; SEQUENCE CHARACTERISTICS:	ucleic	HYPOTHETICAL: NO (9enomic) ANTI-SENSE: NO (ORGINAL) ORGINAL SOURCE:	CREALISM: NOMO Saplens INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8 US-08-579-823A-3	2e-308 Length: 3628.00 Matches: 100.00% Conservative: 5:milarity: 100.00% Mismatches: Milarity: 100.00% Mismatches:	100.00%	SEGS (1-803) X US-U8-5/9-823A-3 (1-2385) QY	21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 4 [1]	41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 6

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Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
                                                                                                                                                                                                                                                                                                                                                     ZIP: 94306
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL IMPORMATION:
APPLICANT: Laus, Reiner
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STATE: CA
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INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene;
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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Mismatches:
                                                                                                                                REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
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Matches:
APPLICATION NUMBER: US/09/344,195
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                                                       APPLICATION NUMBER: US/09/146, FILING DATE: 03-SEPT-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                     NAME: Judge, Linda R. REGISTRATION NUMBER: 42,702
              FILING DATE: 24-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-653) x US-09-344-195-3 (1-2385)
                                                                                                                                                                  TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                                                                                            LENGTH: 2385 base pairs
                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                         PRIOR APPLICATION DATA:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
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Best Local Similarity:
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541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnalaArgH1sCys	Oy 601 ProSerGiyValLysProAspLeuSerTyTweErrolleTrupLysPherDaspGiuGlu 620		; GENERAL INFORMATION: APPLICANT: Cheever, Martin A. APPLICANT: Disis, Mary L. TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu TITLE OF INVENTION: ONCOGENE IS ASSOCIATED	and	STATE: WASHINGTON COUNTRY: USA ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIALE COMPUTER: TBM PC COMPATIALE	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PILING DATE: 01 - APR-1996 CLESSIFICATION - 424 CLESSIFICATION - 424	Key, RON NUMB	; TELEPHONE: (206) 622-4900 ; TELEFAX: (206) 682-6031 ; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 3768 base pairs	ST ST TO TO NA LO	Alignment Scores: 4e-308 . Length: 3768 . Cores 36.368 . Length: 3768 . Length: 3
Oy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProWetCysLys 200 111111111111111111111111111111111	41 AlaAlaGIYCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340	61 IleGlnGluPheAlaGlyCysLysLysIJePheGlySerLeuAlaPheLeuProGluSer 	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	1211 GAGACTCTGGAAGAGCATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT	TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeu\[1]	461 LeuGlySerGlyLeuAlaLeulleHisHisAsnThrHisLeuCysPheValHisThrVal 480 [1451 CCCTGGGACCAGCTTTTTGAACCGCACCAGCTCTGCTCCTGCTGCTGCGCCA 1510 501 GluaspGluCysValGlyGluGlyLeuAlaCySHisGlnLeuCysAlaArgGlyHisCys 520	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540

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Main	Mismatches Indels: Gaps:	(1-376	ArgTrpGlyLeuLeuLe 	ysThrGlyThrAspMetLysLeu	GCACCGGCACAGACATGAAGCTG	euArgHisLeuTyrGlnGlyCys(TOGGCACCTOTACCAGGGCTGC	roThrAsnAlaSerLeuSerPheLeu 	leAlaHisAsnGlnValArgGlnV	TCGCTCACAACCAAGTGAGGCAGG	InLeuPheGluAspAsnTyrAla 	htThrDrovalThrClustingcort	CCACCCCTGTCACAGGGCCTCCC	hrGlulleLeuLysGlyGlyVall	CAGAGATCTTGAAAGGAGGGGTCT	hrileLeuTrpLysAspilePheF 	hrAsnArgSerArgAlaCysHisE	CCAACGCTCTCGGGCCTGCCACC	lyGluSerSerGluAspCysGlns	GAGAGATTCTGAGGATTGTCAGA	rgCysLysGlyProLeuProThrP 	lyProLysHisSerAspCysLeuP 	GCCCCAAGCACTCTGACTGCCTGC	Hiscy	CACTG	luGlyargTyrThrPheGlyalas 	hrAspValGlySerCysThrLeuV
18. (aitty: 100. 2 2	US-08-625-101-	MetGluLeuAlaA] 	AlaSerThr	GCGAGCACC	ThrHisLe			GinglyTyr	CAGGGCTAC				ა —	-0	LeuCysTyr CTCTGCTAC	Le	=5	GlySerAr	SOLDE	AlaGlyG GCCGGTG	AlaAlaGlyCys	GCTGCCGGCTGC	SerGlyIleCys	GTGGCATCTGTG	erMetProAsnP 	yrAsnTyrLeuS

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Sequence 1, Application US/08356786

Patent No. 5877305

GENERAL INFORMATION:
APPLICANT: Huston, James S.

APPLICANT: Oppermann, Hermann
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                                                                                                    ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz,
STREET: Exchange Place, 53 State Street
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SOFWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                   Binding
                                                                                                                                                                                                                                                                                                                       AFPLICATION NUMBER: US/US/350,700
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0.07/831,967
FILING DATE: 0.6-FEB-1992
ATONNEY/ACBT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: CRP-053
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDRES: single
                                  Biosynthetic
Marker
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosyni
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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SOFTWARE: PAtentI
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LeuGlySerGlyLeualaLeulleHisHisAsnThrHisLeuCysPheValHisThrVal 	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 	GluaspGlucysValGlyGluGlyLeualaCysHisGlnLeuCysAlaArgGlyHisCys 	Trp61yPro61yProThrG1nCysValAsnCysSerG1nPheLeuArgG1yG1nG1uCys 	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgH1SCys 	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 	AlaAspGInCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 	ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653 	US/09048804 Bennett, Allan Lipton, Lois M. Witters Bennett, Allan Lipton, Lois M. Witters HUMAN HER-2 EXPRESSION 10 28. SK Washburn Kurtz Mackiewicz & No. 5968748ris The Brance - 46th Floor WH: Wh diskette Compatible Proso/Ms. Dos Release #1.0, Version #1.25 AATA: US/09/048,804 AITIN: AATA AATA AATA AATA SK SA
		GluaspGluCysValGlyGl 	TrpGlyProGlyProThrGl 							lication 748 ATION: C. Frank ENTION: ENTION: CE ADDRES: CO ADDRES:
461	481	501	521	541	561 1681	581	601	621 1861	641	RESULT 6 US-09-048-804-1 Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl TITLE OF INVE SEGUENCE SEGUENCE CORRESPONDENC ADDRESSEE: CONTRY: Phil STATE: Phil
Oy Dp	Oy Dp	Qy Dp	Qy Db	Qy Db	Q Q	Qy Db	Qy Db	5 A	Oy Dp	8 D

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                                                            Conservative:
Mismatches:
Indels:
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Matches:
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                                                   5.19e-308
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100.008
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     pairs
    EENGTH: 4473 base pairs:
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
ANTI-SENSE: No
SEQUENCE CHARACTERISTICS:
                                                             Percent Similarity:
Best Local Similarity:
                                             Alignment Scores:
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(1-653) x US-09-056-105-26
                      US-09-056-105-26; Sequence 26, Application; Patent No. 6287569
                                                                                                       ; ORGANISM: Homo sapiens
US-09-056-105-26
                                                                                                                           rercent Similarity: ·
Best Local Similarity: ·
Query Match:
                          Sequence 26, Applicate Patent No. 6287569 GENERAL INFORMATION:
                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                         SEQ ID NO 26
LENGTH: 4473
                                                                                                  TYPE: DNA
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                                                                                GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
                                                                                                               SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
        LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu
                                                                                              PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
                                                                                                                                  AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla
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                                                                           IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: KIPSC, THOMAS J.
TITLE OF INVENTION: VACCINES WITH ENHANCED I
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
MUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
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                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414
TELECOMUNICATION INFORMATION:
TELEPHONE: 404-688-9890
         ZIP: 30300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"ANDITMER: IBM PC COMPATIBLE
                                                                                                                                                                            5.29e-308
3628.00
100.00%
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                                                                                                                  INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 4530 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                  ; TOPOLOGY: linear
US-08-645-865-9
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  30303
                                                                                                                                                                    Alignment Scores:
Pred. No.:
  COUNTRY:
ZIP: 3030
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Query Match: 100.00% Indels: 0 DB: 4 Gaps: 0	SEQ3 (1-653) x US-09-167-322-4 (1-4530) Qy	21 AlaSerThrGlnValCysThrGlyThrAspWetLysLeuArgLeuProAlaSerProGlu	Db 211 GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGTCCCTGCCGAGG 270 . Qy 41 ThrHisLeuaspMetLeuargHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60	Db 271 ACCCACCTGACATGCTCCGCCACCTCTACCAGGGTGCTGGTGGTGGTGGAAACCTG 330 Ov 61 GluLeuThrTvrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80	331 GAACTCACCTACCCACTATCATCACTGCTTCCTTCCTTCC	Qy 81 GlnGlyTyrValLeuIlealaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100	Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120	Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140 	Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160 	Oy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180	Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200 	Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220	Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240	Qy 241 AlaAlaGlyCySThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280	Qy 281 SerMetBroAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 	Qy 321 GluvalThralaGluaspGlyThrGlnargCysGluLysCysSerLysProCysAlaArg 340
Db 1771 GTGGAGGAATGCCGAGGGGTCCCCCAGGGAGTATGTGAATGCCAGGCACTGT 1830	Oy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580		Oy 601 ProSerGiyValLysProAspleuSerTyrMetProf1EfrpLysPheProAspGluGlu 620 	Oy 621 GlyalaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653	Db 2071 GGCTGCCCGGGGGAGGAGCCAGCCTCTGACGTCC 2109 RESULT 10 INS-A04-167-322-4	ppli 6515 ORMA	AFFLICANT: Allegementy University of the Health Sciences, Halpern, Michael S. England, James M. TITLE OF INVENTION: CANCER VACCINE	CORRESPONDENCE ADDRESS: 14 CORRESPONDENCE ADDRESS: STREET: Suite 1800, Two Penn Center Plaza	STATE: PA STATE: PA COUNTRY: USA ZIP: 19102	CONTOUR TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: DatentIn Palease #1 0 Varcion #1 20	TYTION DATA: NUMBER: US/09/167,322 NUMBER: US/09/167,322	PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US97/00582 FILING DATE: ANTODAMETON:	REGISTRATION NUMBER: 30,480 REGISTRATION NUMBER: 7933-33 PC	IELECTRICATION IN FORMATION: TELEPHONE: (215) 568-8383 TELEFAX: (215) 568-5549 INFORMATION FOR SEQ ID NO: 4:	LENGTH: 4530 base pairs TYPE: nucleic acid STRANDENESS: single	DESCRI	Alignment Scores: 5.29e-308 Length: 4530 Fred. No.: 3628.00 Matches: 653 Score: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0

CURRENT SOFTWAR SOFTWAR SEQ ID R TENGT TYPE: TYPE: NAME/F NAME/F NAME/F NAME/F NAME/F NAME/F NAME/F	Alignment Pred. No.: Score: Percent Si Best Local Ouery Match	SEQ3 (1-65 QY Db	d ç d	0	00 OX OX OX	90 O	oy oy	90 60 60 60
Oy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360	Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSeralaTrpProAspSerLeuPro 420 Db 1351 GAGACTCTGGAAGAGTCACAGGTTACTTACATCTCAGCATGGCCGACAGCCTGCCT	Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgGlu 460 Db	Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500 Db 11	521 TrpGlyProGlyProThrGllnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 Db	Qy 601 ProSerGlyvalLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620 Db 111111111111111111111111111111111111	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653	RESULT 11 US-09-527-487-1 ; Sequence 1, Application US/09527487 ; Patent No. 6528060 ; GARLEN INFORMATION: ; APPLICANT: Nicolette, Charles ; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES ; FILE REPERENCE: 126881309200 ; CURRENT APPLICATION NUMBER: US/09/527,487

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NT FILING DATE: 2000-03-16
R OF SEQ ID NOS: 9
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181 LeuThrLeuIleAspT 	201 GlySerArgCysTrpG] 	221 AlaGlyGlyCysAlaAı 	241 AlaaladlyCysThrGl 	261 SerGlylleCysGluLe 	281 SerMetProAsnProGl 	301 TyrAsnTyrLeuserTh 	321 GluValThrAlaGluAs 	341 ValcysTyrGlyLeuGl 	361 IleGlnGluPhealaGl 	381 PheaspGlyaspFroAl 	401 GluThrLeuGluGluIl 	421 AspLeuSerValPheGl 	441 TyrSerLeuThrLeuGl 	461 LeuGlyserGlyLeuAl. 	481 ProTrpAspGlnLeuPh 	501 GluAspGluCysValGly 	521 TrpGlyProGlyProTh
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1831 TTGCCGTGCCACAGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 1890
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
SOFTWARE: Winbatin (Genentech)
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
CLASSIFICATION DATA:
APPLICATION DATA:
13.DEC-1994
LIUNG DATE: 13.DEC-1994
LIUNG DATE: 13.DEC-1994
APPLICATION NUMBER: 08/48346
FILING DATE: 15.APR-1993
LIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JICANT: Hudziak, Robert M.
JICANT: Shepard, H. Michael
LICANT: Ullrich, Axel
E. OF INVENTION: HER2 EXTRACELLULAR DOMAIN
BER OF SEQUENCES: 2
BERPONDENCE ADDRESS:
ODRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRESSEE: Genentech, Inc.
REET: 460 Point San Bruno Blvd
TY: South San Francisco
ATE: California
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No. 6015567
L INFORMATION:
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LING DATE: 19-MAY-1989
RNEY/AGENT INFORMATION:
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EGISTRATION NIMBER: 00,000
EFERENCE/DOCKET NUMBER: 554C
ECOMMUNICATION INFORMATION:
ELEPHONE: 415/255-1994
ELEFAX: 415/952-9881
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LENGTH: 1872 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
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US-08-422-734-2
; Sequence 2, Application U:
; Patent No. 6333169
; GENERAL INFORMATION:
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Mismatches:
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ValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGlyAsp
                GUGCGAGGCACCCAGCUCUUGAGGACAACUAUGCCCUGGCCGUGCUAGACAAUGGAGAC
                                                                                    LeuArgSerLeuThrGluIleLeuLysGlyGlyWalLeuIleGlnArgAsnProGlnLeu
                                                                                             CysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeu
                                                                                                                                    AlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHisSer
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Matches:
Conservative:
Mismatches:
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                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: 1BM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genemtech)
                    HERZ EXTRACELLULAR
                                                                                                                                                                   APPLICATION NUMBER: US/08/422,734
PILING DATE:
CLASSIFICATION 435
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/422108
FILING DATE: 14-APC-1995
APPLICATION NUMBER: 08/355460
FILING DATE: 13-DEC-1994
APPLICATION NUMBER: 08/355460
FILING DATE: 13-DEC-1994
APPLICATION NUMBER: 08/48346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354319
FILING DATE: 19-ARX-1989
ATTORNEY APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAX-1989
                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                              554C2D1
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   H. Michael
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REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 554
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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3471.00
99.84%
99.84%
APPLICANT: Shepard, H. Mic
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HERZ E.
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                              DATA:
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                                                                                                                                                             CURRENT APPLICATION
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                                                                                           USA
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                                                                                                  94080
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                                                                                         COUNTRY:
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Best Local Similarity:
                                       TOPOLOGY:
US-08-229-515A-14
                                                                     Alignment Scores:
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                                                                                                                                                  GlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCysVal
                                                                                                                     Sequence 14, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
CUTY: Action a
COUNTRY: usa
21P: 30303
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/COCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-9880
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US-08-229-515A-14
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                                                                                                           Conservative:
Mismatches:
                                                                                        Length:
Matches:
                                                                                                                                     Indels:
                                                                                                                                                                     SEQ3 (1-653) x US-08-229-515A-14 (1-3955)
                                                                                       2.54e-262
3106.00
90.21%
85.32%
85.61%
        LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
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Oct 17

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| AATGTCCAGGAGTTTGATGGCTGCAAGAACATCTTTGGGAGCCTGGCATTTTTGCCGGAG
                                                                                                                                                                            ProTyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsn
                                           ValProTrpAspGlnLeuPheArgAsnProHisGlnalaLeuLeuHisThrAlaAsnArg
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BU150809 AGENCOURT

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BF984645 602309702

AN057736 wx02h09.x

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                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-G-Cqqn2_LJ/USPPC_spool_pP/HOLLERN480/runat_15102003_131913_20548/app_query.fasta_1.4685
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Copyright (c) 1993 - 2003 Compugen Ltd
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ALIGNMENTS

BE065758 RC2-BT031 BI557977 603236665 BG991986 MR2-HT116

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447 995 1201 450 508 660 455

499 499 1057 486

em_esthum:*

em_estba:* em_estin:* em_estmu:*

EST:*

Database

em_estro:* em_htc:* gb_estl:*

em_estov:* em_estpl:*

AK031099 4323 bp mRNA linear HTC 05-DEC-2002 Mus musculus 13 days embryo forelimb cDNA, RIKBN full-length enriched library, clone:5930404N10 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived AK031099 AK031099. I GI:26082143 HTC; CAP trapper. Mus musculus (house mouse) Mus musculus chouse mouse) Butataca; Craniata; Vertebrata; Euteleostomi; RESULT 1 AK031099 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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em_gss_pro: em_gss_rod:

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em_estom:*

em_estfun:*

gb_est3:* gb_est4:* gb_est5:* gb_est2:* gb_htc:*

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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of 60/700 full-length cDNAs

is Adachi, J. Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Harashida, K., Harat, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kaya, S., Kurihara, C., Matayama, T., Miyazaki, M., Namara, J., Miyazaki, M., Ohno, M., Ohsato, N., Okaato, N., Satto, R., Sattoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, Y., Sattoh, M., Shibata, K., Shibata, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi, N., Ishili,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshik,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 409 (6821), 685-690 (2001)
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                                                                                  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute

Muramatsu, M. and Hayashizaki, Y.

TITLE JOURNAL

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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
CONA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
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Please visit our web site for further details.
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Conservative:
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Š Š	160 GlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeu 179 	dy Db	520 CysTrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGlu 539
3 & 1	AlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCys	Qy	540 CysValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHis 559
g & 1	rval 	Qy	560 CysLeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyPro 579
3 o	CysAlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisG	δλ	580 GlualaaspGlnCysValalaCysAlaHisTyrLysAspProProPheCysValalaarg 599
o o	CysalaalaGlyCysThrGlyProLySH\sSerAspCysLeualaCysLeuHisPheAsn 2 	Oy Dp	600 CysProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGlu 619
Qy Db	HisserGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPhe 2 	ζζ	620 GluGlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAsp 639
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oy O	340 ArgvalCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAla 359 	ko da	2
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oy O	nval 39 AGTG 12	Qy	ATCCCAGATGGGGAGAACGTGAAAATCCCCGTGGCCATCAAGGTGTTGAGGGAAAACACA 23
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6 6 7	480 ValProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArg 499 	ර් අ	652
0y	500 ProGluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHis 519 :::	Oy Dp	652 652 2628 AAGATTACCGACTTCGGCTGGCTGCTGCACATTGATGAGACTGAATACCATGCA 2687

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GEG GATGGGGGCAAGCTGCCCATCAAGTGGATGCCATTGGAATCTATTCTCAGACGCGGTTC GEG GATGGGGGCAAGCTGCCCATCAAGTGGATGCCATTGGAATCTATTCTCAGACGCGGTTC GEG CACCACACAGTGGTGTGGAGCTATGGTGACTTGTGGAAGCTGATGACTTTGGG GEG CACCACACAGTGGTGTGTGGAGCTTGGTGACTTGTGGAGAAGGAGAAGA GEG CACCACACCTCCACACTCCACCACCACGAGACCACTCATGTTGG GEG CACCACACCTCCACACTCCACCACCACACACACACACAC	TITLE	JOURNAL	MEDLINE	REFERENCE	AOIDORA					 		TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS	TITLE JOURNAL REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	041000
			GATGGGGGCAAGGTGCCCATCAAGTGGCATTGGAATCTATTCTCAGACGCCGGTTC		ACCCATCAGAGTGATGTGGAGCTATGGTGTGACTGTGGGAGCTGATGACCTTTGGG		GACAAACCTTACGATGGGATCCCAGCTCGGGAGATCCCTGATTTGCTGGAGAAGGGAGAA		CGCCTACCTCAGCCTCCAATCTGCACCATCGACGTCTACATGATCATGGTCAAATGTTGG	ATGATTGACTCCGAATGTCGCCCGAGATTCCGGGAGTTGGTATCAGAATTCTCCCGTATG		LeuaspSerThrPheTyrArgSerLeuLeuGluaspAspAspMetGlyAspLeuValasp :::	AlaGluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAla		AK083669 4463 bp mRNA linear NN Mus musculus 9 days embryo whole body cDNA, RIKEN fu enriched library, clone:D030063812 product:v-erb-b2 leukemia viral oncogene homolog 2, neuro/glioblaston oncogene homolog (avian), full insert sequence.	Σ		Carnir High-e Meth. 992792 103496	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)	

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Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tomaru,A., Toya,T., Yasunishi,A.,
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and Genome Science Laboratory in RIKEN.
Animal Research in Riken contributed to
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1384 multicapillary sequencer
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Alignment Score Pred. No.:	es:	1.9e-246	Length:	4463	
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1 4 8 4 A 8 A 8	4etGluLer 	AlaAlaLeuCys/ GCGCCTGGTGC	rgTrpGlyLeuLeuLe :GTTGGGGGTTCCTCC	MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAl 	La 20
21 A 108 G	AlaSerThr CGGGTACC	GlnValCysThr(lyThraspMetLysLe 	AlaSerThrGlnValCysThrGlyThrAspMetLySLeuArgLeuProAlaSerProGl 	lu 40
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61 G 1 228 G	3luLeuThr AGCTTACC	TyrLeuProThr/ TACCTGCCCGCC/	snalaSerLeuSerP arGCCAGCCTCTCATJ	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 	11 80 11 7 12 287
81 G 288 C	SlnGlyTyr AGGGATAC	:ValLeuIleAlaE ::: ATGCTCATCGCTC	lisasnGlnValArgG] ::: ::: :acaaccgagtgaaac	GInGlyTyrValLeuIleAlaHisAsnGInValArgGInValProLeuGlnArgLeuArg 	rg 100 - 3C 347
101 I 1 348 A	[levalarg \TCGTGAGA	JGlyThrGlnLeuk 	heGluAspAsnTyrA TTGAGGACAAGTATGC	IleValargGlyThrGlnLeuPheGluAspasnTyralaLeuAlaValLeuAspasnGly 	ly 120 3A 407
121 A 108 G	AspProLeu 	ASnAsnThri ::: GACAACGTCACC	hrProValThrGlyA] 	ASPProLeuAsnAsn ThrThrProValThrGlyAlaSerProGlyGlyLeuArgGlu 	lu 139 G 467
140 I 468 C	SeuGlnLeu 	ArgSerLeuThr(luIleLeuLysGlyG] 	LeuGinLeuArgSerLeuThrGluïleLeuLySClyGlyValLeuïleGlnArgAsnPro 	TO 159
160 G 1 528 C	lllllll Agcrerge	TyrGlnAspThr] TACCAGGACATG	leLeuTrpLysAspl] :: :TTTTGTGGAAGGATG1	GlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeu 	au 179 G 587
180 A 588	AlaLeuThr - crccrgrc	LeuIleAspThr? ::: :GACATGGACACC?	snArgSerArgAlaC) 	AlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCys :::	/s 199 SC 647
200 I 648 A	JysGlyser ::: AAGACAAT	: 	iluSerSerGluAspC) AGAGTCCTGAAGACTC	LysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrVal :::	11 219 :: :C 707
220 C	ysalagly GTACTAGT	/GlyCysAlaArg(ystysGlyProteuPr GCAAGGGCCGGCTGCC	CysalaglyglyCysalaArgCysLysGlyProLeuProThraspCysCysHisGluGln 	In 239
240 C	CysAlaAla TGTGCTGCA	GlyCysThrGlyE	roLysHisSerAspC) 	CysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsn 	sn 259
	lisSerGly	/IleCysGluLeu	isCysProAlaLeuV∂	HisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPhe	27

GluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCys SerPheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnVal GluLeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThr ValProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArg uGluGlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAs 14.88

652 2028 GGGCGTCCTGTTGTTCCTGATCATGGTGGTCGTTGGATCCTAATCAACGAGGGG 652 2088 ACAGAAGATCCGGAAGTATACCATGCTTGGTGGTGGTGGTGGAGGCGTGGGGGGGG	TCCTAATCAACGAAGGG 2087 QY QY	656 uAspLeuGlyProAlaSerProLeuAspS
2028 GGGCGTCCTGTTGTTCCTGATCATAGTGGTGGTCATTGG 652	2087 652 2147 652 2207 652 2267 652 2327	
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148 ACAGAAGATCCGGAAGTATACCATGCGTAGGCTGCACAGAGAAGTATACCATGCGTAGGCTGCACAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG	2147 652 2207 652 2267 652 2327	
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652	652 2267 652 2327 652	3228 CCCAGACCCTGCCCTAGGTACTGGGAGCA
2208 CTCGCTCCAGCTGGAGCCGCTGACGCCCCAGTGGAGC 652	2267 652 2327 652	
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2268 GCGGATCCTAAAGGAGCAGAGCTAAGGAAAGGTGAAGGTG652 2328 CACTGTCTACAAGGGCATCTGGATCCCAGATGGGGAGAA(652	2327	library, full inse
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2328 CACTGTCTACAAGGCATCTGGATCCCAGATGGGGAGAAA 652		Mus
652	ORGANISM ORGANISM	SM Mus musculus Eukaryota; Metazoa; Chordata;
2388 CAAGGTGTTGAGGGAAACACATCTCCTAAAGCTAACAA 652	REFERENCE	
652	2447	
2448 CGTCATGGCTGGTGTGGGTTCTCCATATGTCTCCGCCTG 652	JOURNAL MEDILINE MEDILINE	
652	TGGGCATCTGCCTGACATC 2507 REFERENCE	
2508 CACAGTGCAGCTGGACACAGCTTATGCCCTATGCCTGG 652	AOTHOR AUTHOR	
652	2567	Normalization and subtraction or prepare full-length cDNA librar
2568 ACACCGAGGTCGCTTAGGCTCCCAGGACCTGCTCAACTG 652	JOURNAL MEDLINE MEDLINE	
GATGAGCTACCTGGAGG AGTCAAGAGTCCCAACC TGATGAGACTGAATACC	GTGTTCAGATTGCCAAGG 2627 REFERENCE	
GATGAGCTACCTGGAGG	AUTHOR AUTHOR	
652	TAGCTGCCCGAAACGTGCT 2687	Sumi, N., Isnii, Y., Nakamura, S., Yamamoto, R., Matsumoto, H., Saka
2688 AGTCAAGATCCCAACCACGTCAAGATTACCGACTTCGGC 652	652	rujiwake, S., indue, N., iogawa, I Yoneda Y., Ishikawa, T., Ozawa, K
652	TGGCACGCCTGCTGGACAT 2747	OKazaki,i., Muramatsu,M., Inoue RIKEN integrated sequence analy:
2748 IGAIGAGACTGAATACCAIGCAGAIGGGGGCAAGGIGCCC 652	JOURNAL 652	Sequencing pipeline with 364 mu.
652	2807	
2808 ATCTATTCTCAGACGCCGGTTCACCCCATCAGAGTGATGT	REFERENCE 652 AUTHORS	
	GGAGCTATGGTGTGACTGT 2867	Arakawa,T., Hara,A., Fuku Aizawa,K., Izawa,M., Nish
652	652	Saito,T., Okazakı,Y., Gojo Kadota,K., Matsuda,H., Asl
2868 GTGGGAGCTGATGACCTTTGGGGCCCAAACCTTACGATGGGATCCCAGCTCGGGAGATCCC	TCCCAGCTCGGGAGATCCC 2927	Fleischmann, W., Gaasterlar Kuehl, P., Lewis, S., Matsuc
652	652	Quackenbush,J., Schriml,L. Wagner,L., Washio,T., Saka
2928 TGATTTGCTGGAGAAGGGAGAACGCCTACCTCAGCCTCCAATCTGCACCATCGACGTCTA	TCTGCACCATCGACGTCTA 2987	Baldarelli, R., Barsh, G., Blake, Carninci, P., de Bonaldo, M.F., B
652		Fletcher, C., Fujita, M., Ga Hofmann, M., Hume, D.A., Kan

bata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Shi,Y., Konno,H., Adachi,J., Fukuda,S.,
K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
OTI,T., Bono,H., Kasukawa,T., Saito,R.,
Urner,M., Batalov,S., Casavant,T.,
'T., Gissi,C., King,B., Kochiwa,H.,
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'K., Okido,T., Furuno,M., Aono,H.,
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'ya,M., Lee,M., Sasaki,H., ,K., Nagaoka,S., Sasaki,N., Carninci,P., K., Kitsunai,T., Tashiro,H., Itoh,M., S., Hazama,M., Nishine,T., Harada,A., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Wa,Y., Izawa,M., Ohara,E., Watchiki,M., Wa,K., Tanaka,T., Matsuura,S., Kawai,J., noue,Y., Kira,A. and Hayashizaki,Y. nalysis (RISA) system--384-format 4 multicapillary sequencer SerThrPheTyrArgSerLeuLeudluAspAs 676 p mRNA linear HTC 05-DEC-2002 cDNA, RIKEN full-length enriched luct:epidermal growth factor receptor, Lsu,N., Sugahara,Y., Shibata,K., Muramatsu,M. and Hayashizaki,Y. of cap-trapper selected chNAs to aries for rapid discovery of new genes 0 (2000) GACCCCCAGCGCTTTGTGGTCATCCAGACGA 3107 959 Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus ---SerGlnAsnGl ACAGCCCACCGCAGACACCGC 3276 MetValHisHisArgHisArg 712 NA cloning

JOURNAL

TITLE

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Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Exploration Research (EXERN), Laboratory for Genome
Exploration Research (EXERN), Laboratory for Genome
Exploration Research (EXERN), Laboratory for Genome
RIKEN Yokohama Institute; 1--22 Submiro-cho, Tsurumi-ku, Yokohama,
URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Fursas Visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Yoyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 (111-1ength cDNAs Nature 420, 563-573 (2002)

( bases I to 2456)
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                                                                                                               Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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COMMENT

CDS

FEATURES

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KVCNGIGIGEFKDTLSINATNIKHFKYCTAISGDLHILPVAFKGDSFTRTPPLDPREL
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4 CysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMetPro 283 ::: ::: 3 TGCAAGGACACCTGCCCACCACGACGTGTACAACCCCACCACCTATCAGATGGATG	4 ASDPrOGIUGIYARGTYrThrPheGIyAlaSerCysValThrAlaCysPrOTyrAsnTyr 303	4 LeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGlnGluValThr 323 :::	4 AlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArgValCysTyr 343 ::::: :: GAAGAAGATGGCATCCGCAAGTGTAAAAAATGTGATGGGCCCTGTCGCAAAGTTTGTAAT 1269	4 GlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsnIleGlnGlu 363 ::: ::: GGCATAGGCATTGGTGAATTTAAAGACACACTCTCCATAAATGCTACAAACATCAAACAC 1329	4 O	4 AspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPheGluThrLeu 403 ::	4 GlugluileThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuProAspLeuSer 423 :::	4 ValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAlaTyrSerLeu 443 	4 ThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGluLeuGlySer 463 :::	4 GlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrValProTrpAsp 483 ::: ::: :: ::	4 GlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgProGluAspGlu 503 :::	4 CysvalGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCysTrpGlyPro 523	4 GlyProThrGlnCysValAsnCySSerGlnPheLeuArgGlyGlnGluCysValGluGlu 543 	4 CysargValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCysLeuProCys 563 ::: ::: ::: TGCAACATCCTGGAGGGGAACCAAGGGAGTTTGTGGAAATTCTGAATGCATCCAGTGC 1929	4 HisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAlaAspGln 583	4 CysvalalaCysalaHisTyrLysAspProProPheCysValAlaArgCysProSerGly 603 	4 ValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGluGlyAlacys 623 :::::::::::::::::::::::::::::::::::
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Guackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolunga, N., Pletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, T., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wayshazaki, Y., Rawaji, H., Kohtsuki, S. and Hayashizaki, Y., Suzuki, M., Runctional annotation of a full-length mouse cDNA collection Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., NishineT., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kahiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) CACCTATGCCACGCCAACTGTACCTATGGATGTGCTGGGCCCAGGTCTTCAAGGATGTGAA 2166 1167 GTGTGGCCATCTGGGTACGTTCAATGGCAGTGGATCTTAAAGACCTTTTGGATCTAAGAC 2226 Mus musculus adult male liver cDNA, RIKEN full-length enriched full insert sequence.
AKO04883 genes ---ArgAlaSerProLeuThrSer 653 624 GlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLysGlyCys--- 642 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 2227 CAGAAGCCATCTCTGACTCCCTCTCACCT-----TCCAGTTCTTCCAAATCCTC 2277 672 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramacau, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000) 654 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeu Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Weth. Enzymol. 303, 19-44 (1999) 99279253 Mus musculus (house mouse) Mus musculus -----ProAlaGluGln----AK004883.1 GI:12836403 HTC; CAP trapper. 10349636 11076861 2107 643 LOCUS DEFINITION ORGANISM MEDLINE PUBMED MEDLINE PUBMED REFERENCE AUTHORS MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS REFERENCE AUTHORS JOURNAL JOURNAL RESULT 4 AK004883 TITLE TITLE TITLE g δ q δý

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Submitted (10-JUU-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reseggsc.riken.go.jp,) Please visit our web site (http://genome.gsc.riken.go.jp,) for further details.
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/dev_stage="adult"
282. .2249
                                                                                                             Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                       The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I \& II Team.
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1. 2662
/organism="Mus musculus"
(6821), 685-690 (2001)
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/sex="male"
                                                                                                                                                   Nature 420, 563-573 (2002)
6 (bases 1 to 2662)
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LCSSEGCWGPEPRDCYSCONYSRGRECYEKONILEGEPREFYENSECIQCHPECLPQA
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Itawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Osjobon, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavánt, T., Radota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavánt, T., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchionni, L., Mashima, J., Mazzacelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Willming, L., Waynshaw-Boris, A., Wang, K.H., Weitz, C., Whittaker, C., Willining, L., Waynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. AK004944 11near HTC 05-DEC-2002 Mus musculus adult male liver CDNA, RIKEN full-length enriched library, clone:1300008123 product:epidermal growth factor receptor, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishili,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wathiki,M., Yonaca,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000) 2193 GTGTGGCCATCTGGGTACGTTCAATGGCAGTGGATCTTAAAGACCTTTTGGATCTAAGAC 2252 Euteleostomi; The FANTOM Consortium and the RIKEN Genome Exploration Research Murinae; Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArgSerLeu Chordata; Craniata; Vertebrata; E Rodentia; Sciurognathi; Muridae; noi,P. and Hayashizaki,Y. sfficiency full-length cDNA cloning Enzymol. 303, 19-44 (1999) Eutheria; Rodentia; Mus musculus (house mouse) AK004944.1 GI:12836511 full insert sequence. Eukaryota; Metazoa;

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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakwa,T., Bono,H., Carninoi,P., Fukuda,S., Fukunishi,Y.,
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Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi, ku, Yokohama,
Kanagawa 230-0045, Japan (F-mail:genome-resegsc.riken.go.jp,
Pax:81-45-503-9225,
Pax:81-45-503-9225,
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                  Nature 420, 563-573 (
6 (bases 1 to 2936)
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                                                                                                                                                       PheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPheAspGly 383
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424 ValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAlaTyrSerLeu
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964 bp mRNA linear EST 03-SEP-2002 AGENCOURT_8118591 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6180101 5', mRNA sequence.
2186 GTGTGGCCATCTGGGTACGTTCAATGGCAGTGGATCTTAAAGACCTTTTGGATCTAAGAC 2245
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Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 964)

NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs_r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.lln.gov
Plate: LLAM13562 row: f column: 06
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//once="Vector: pCMV-SPORT6 (Life Technologies); Sit
Not1: Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
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287
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/lab_host="DH10B"
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Matches:
Conservative:
Mismatches:
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Gaps:
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High quality sequence stop: 529.
Location/Qualifiers
1. :964
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                             BU150809
BU150809,1 GI:22664341
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474 302 362 514 422

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662

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722 634 782 652 842 652

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1203 GCTGGTGTGGGGTTCTCCATATGTGTCCCGCCTCCTGGGCATCTGCCTGACATCCACAGTG 1262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1143 TTGAGGGAAAACACATCTCCTAAAGCTAACAAAGAAATCCTAGATGAAGCGTACGTCATG 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           963 GAGCTGGTGGAGCCGCTGACGCCCAGTGGAGCTGTGCCCAACCAGGCTCAGATGCGGATC 1022
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                                                                                                                                                       123 TGGCCAGAGAGCTTCCAAGACCTCAGTGTCTTCCAGAACCTTCGGGTCATTCGGGGACGG
                                                        CysPheValHisThrValProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeu
                                                                                                                                                                                                                                                                                                          303 TGCTTTGTAAACACTGTACCTTGGGACCAGCTCTTCCGGAACCCGCACCAGGCCCTACTC
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                                                                                                         595 PheCysValAlaArgCysProSerGlyValLysProAspLeuSerTyrMetFroIleTrp
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// (FOOLE) id="BAC27442.1"
// (Ab__XET=28139.7"
// (Ab__XET=28139.7")
// (A
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LSPGKNGVVKDVFAFGGAVENPEXLAPRAGTASQPHPSPAFSPAFDNLYYWDQNSSEQ
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                                    Yokohama,
                                                                                                                      CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product; putative v-erb-loz erythroblastic leukemia viral oncogene homolog neurc/glioblastoma derived oncogene homolog (avian) (MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%,
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Conservative:
Mismatches:
Indels:
Gaps:
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/mol_type="mmNA"
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/lab_host="DH10B (phage-resistant)"
/clone="lorgan: small intestine; Vector: pCMV-SPORT6;
/clone="lorgan: small intestine; Ve
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can library through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov n column: 04 High quality sequence stop: 637. Location/Qualifiers
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AGENCOURT_6566679 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5736771
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                      CAGCTGGTGACACAGCTTATGCCCTATGGCTGCCTTCTGGACCATGTCCGAGAACACCGA
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
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Qy	294 SerCysValThrAlaCysProTyrAsnTyrLeuSerThrAspValGlySerCysThrLeu 313
qq	732 AGCTGTGTGACTGCCTGTCCCTACAC-TACCTTTCTACGGACGTGGGATCCTGCACCCTC 790
٥٧ م	314 ValCysProLeuHisAsnGlnGluValThrAlaGluAspGlyThr-GlnArgCysGlu-L 333
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RESULT 9 AU140362 LOCUS DEFINITION	z
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	. X
REFERENCE AUTHORS	Eukar Mamma 1 (t
TITLE	Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y. and HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y.,
JOURNAL COMMENT	AL
	Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975
	Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
FEATURES SOU	rce
BASE COU	JUNT 149 a
Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Alignment Scores: 5.09e-101 Length: 757 Pred. No.: 1364.00 Matches: 246 Score: 1364.08 Conservative: 0 Best Local Similarity: 98.40% Mismatches: 4 Query Match: 98.50% Indels: 0 DB: 9
SEQ7 (1-	(1-712) x AU140362 (1-757)
Qy	332 GluLySCySSerLySProCySAlaArgValCySTyrGlyLeuGlyMetGluHisLeuArg 351

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808 bp mRNA linear EST 14-NOV-2002
AGENCOURT_10810594 MAPCL Homo sapiens cDNA clone IMAGE:6722008 5',
CA489534
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Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 808)
11 (hartp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
443 ATCTCAGCATGGCCGGACAGCCTGCCTGACCTCAGCGTCTTCCAGAACCTGCAAGTAATC
                                                                                                                                                                                                                                                          452 TrpLeuGlyLeuArgSerLeuArgGluLeuGlySerGlyLeuAlaLeuIleHisHisAsn
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                                                    GlySerLeuAlaPheLeuProGluSerPheAspGlyAspProAlaSerAsnThrAlaPro
                                                                                                       LeuGlnProGluGlnLeuGlnValPheGluThrLeuGluGluIleThrGlyTyrLeuTyr
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenciap by: Agencourt Bioscience Corporation
Clone distribution: MG clone distribution information con lifound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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seq7.rst

662

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 894)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.lini.gov
Plate: LLCW/SB row: e column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE746725 894 bp mRNA linear EST 15-SEP-2000 601579159F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3927927 5',
                                                                                                                        371 heGlySerLeuAlaPheLeuPro---GluSerPheAspGlyAspPro---AlaSerAsnT 389
                                                                                                                                                                                                                                                                                    ::|||:::
723 GGGGAGCCTGGCAATTTCTGCCCGGAAAAACTTTTGATGGGGAACCCAACCTCCCAACA 782
894
261
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Gaps:
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High quality sequence stop: 762.
Location/Qualifiers
1.894
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                                                                                                                                                                                                                                                                                                                                                                                                             783 CTGGCCCCGGTTCCAGCCCAAA 805
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1293.00
85.76%
84.47%
32.70%
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Homo sapiens
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BE746725
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Pred. No.:
                                                                                                                        353
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BE746725
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JOURNAL
COMMENT
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//octe="Vector: pcMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
//octe="Vector: pcMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
//octe="Vector: pcMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
//octe="Vector of the priming method: oligo-dr. Average insert size: 1800 bp. Library amplification: 26,000 fold.
//octe for the Pastan: Discovery of new breast cancer senceding membrane and secreted proteins.
//octe for the proteins of the proteins
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247
8
8
6
                                                                                                                                           /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
   row: a column: 16
                                                                                               1. .808
/organism="Homo sapiens"
                            High quality sequence stop: 5 Location/Qualifiers
                                                                                                                                                                                                                                                                          , LNCap"
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ORIGIN
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  ORGANISM
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AUTHORS
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Pred. No.:
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                                              301
                                                                                                                                                                                                       361
                   61
                                                                                                                                                                                   662 CATCAGCTTGGCTGGGGCTGCGCTCACTTGAGTGGAACTTGGGGGCAGTGGACTGGCC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnProHisGlnAlaLeuLeuHisThrAlaAsnArgProGluAspGluCysValGlyGlu
468 IleHisHisAsnThrHisLeuCysPheValHisThrValProTrpAspGlnLeuPheArg
                                                                                                                                                          AlaProLeuGlnProGluGlnLeuGlnValPheGluThrLeuGluGluIleThrGlyTyr
                                                                                                                                                                                                                                                                                                                                   410 LeuTyrIleSerAlaTrpProAspSerLeuProAspLeuSerValPheGlnAsnLeuGln
                                                                                                                                                                                                                                                                                                                                                                      ValIleArgGlyArgIleLeuHisAsnGlyAlaTyrSerLeuThrLeuGlnGly-LeuGl
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                                                                          AlaLeuValThrTyrAsnThrAspThrPheGluSerMetProAsnProGluGlyArgTyr
                                                                                                             ThrPheGlyAlaSerCysValThrAlaCysProTyrAsnTyrLeuSerThrAspValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          795 bp mRNA linear UJ-M-FYO-cda-e-16-0-UI.r1 NIH_BMAP_FYO Mus musculus (IMAGE: 6826841 5', mRNA sequence. CA328613.1 GI:24546711 EST.
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VERSION
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1...'97
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/lone="organ: Brain; Vector: pXx- Asc; Site_1: EcoR I;
/site_2: Not I: The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pxx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AcGGAGAGAG. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182
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                                                                                                                                                                                                                                                cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be thtp://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Jases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 others
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Conservative:
Mismatches:
Indels:
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238 c 216 a
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                                                                                                                                                      Unpublished
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COT 25-NORMALIZED."
s PLACENTA COT 25-NORMALIZED."
was primed with a NotI-oligo(dT)
enriched, double-strand cDNA was
cloned into the Not I and EcoR V
cloned. Library was normalized."
23 t 46 others 419 alargGlnValProLeuGlnArgLeuAr 100 snTyrAlaLeuAlaValLeuAspAsnGl 120 419 lyalaSerProGlyGlyLeuArgGluLe 140 419 419 laCysHisProCysSerProMetCysLy 200 419 220 euLeuLeuAlaLeuLeuProProGlyAl 20 euSerPheLeuGlnAspIleGlnGluVa 80 |||||||||||| TGTCCTTCCTGCA-GAC------ 419 lyGlyValLeuIleGlnArgAsnProGl 160 spilePheHisLysAsnAsnGlnLeuAl 180 419 euProThrAspCysCysHisGluGlnCy 240 spCysLeuAlaCysLeuHisPheAsnHi 260 419 spCysGlnSerLeuThrArgThrValCy s: /ative: ches:

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Scores:
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sSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGl 280
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Homo sapiens CDNA, mRNA sequence.
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I (bases 1 to 614)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
Unpublished
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                               nGluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaAr
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                                uSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPr
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/716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue manna and cDNA amplification were performed under low stringency conditions."

19 a 198 c 172 g 124 t lothers
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL PRIO260-61199-024-all&t3-1999-11-01&t4-1)
Seq primer: puc 18 forward
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High quality sequence stop: 612.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
E. (Dabases 1 to 613)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Lonpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=Torgan: muscle; Vector: pOTB7; Site_1: ECORI; Site_2: XhOI; cDNA made by oligo-dT priming.
Site_2: XhOI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACAGG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                    AW410534 11NH_MGC_17 Homo sapiens cDNA clone IMAGE:2961635 5',
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www.bio.llnl.gov/bbrp/image/image.html
Plate: LLCM56 row: O coluum: 12
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
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Sequence 118, Appli
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Sequence 46, Appli
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Sequence 119, App
Sequence 124, App
Sequence 1, Appli
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Sequence 95, Appl
Sequence 98, Appl
Sequence 15, Appl
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Sequence in Visualization US/10207498

Publication No. US20030143568al

GENERAL INFORMATION:

APPLICANT: Falizabeth Singer

APPLICANT: David Eisenberg

TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING

TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
FILE REFERENCE: 30448.103-US-U1

CURRENT APPLICATION NUMBER: US/10/207,498

CURRENT FILING DATE: 2002-07-29

PRIOR PADDICATION NUMBER: 60/208,431
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Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
                                                                                                           Sequence 81, Appl
Sequence 32, Appl
Sequence 44, Appl
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US-09-81-132-7

US-09-81-183-9

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US-09-91-133-1

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"MODEL-frame+_p2n.model_DEV=xlp

"G-/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_15102003_131915_20662/app_query.fasta_1.4685
-0-/cgn2_1/USPTO_spool_p/HOLLERAN480/runat_15102003_131915_20662/app_query.fasta_1.4685
-DB=Published_Applications_NA -OFMT-fastap -SUFFIX=rnpb -NINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-blts -START=1 -END=-1 -MATRIX-bloamn62
-TRANS-human40.cdl -LIST=46-OCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-TRANS-human40.cdl -LIST=46-OCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -WODE-LOOPEMT-pt -NORM-ext -HEAPSIZE=500 -MINIEN=0
-MAXLEN-2000000000 -USER-HOLLERAN480_GCN_1_1_397_@runat_15102003_131915_20662
-NCPU-6 -LOPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN _TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                        October 16, 2003, 11:08:07; Search time 735.997 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                      OM protein - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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1 MELAALCRWGLLLALLPPGA.
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Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	ores: larity imilar	: ity:	0 3776.00 67.94% 67.94% 95.50%	Length: Matches: Conservative Mismatches: Indels: Gaps:	3765 712 : 0 0 336 1			QY Db QY
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Qy Db	1 MetG] ATGG	luLeuA AGCTGG	laAlaLeuCys CGGCCTTGTGC	MetGluLeualaalaLeuCysArgTrpGlyLeuLeuLeualaLeuLeuProProGlyala 	euAlaLeuLeuF 	roProGlyAla 	20	Oy Dp
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Qy Db	41 ThrHi 121 ACCC	isLeuA: ACCTGG	spMetLeuArg 	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 	/sGlnValValG 	inglyAsnLeu 	60 180	Qy
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Qy Db	101 IleVa 301 ATTGT	alArgG. TGCGAGG	lyThrGlnLet 	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGl: 	aLeuAlavall 	euAspAsnGly 	120 360	Qy
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Qy Db	221 Alagi 661 GCCGG	lyglyc; TGGCTC	ysalaargCys 	AladiydiyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 	rAspCysCysH :TGACTGCTGCC	isgluglncys ATGAGCAGTGT	240 720	Qy
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Qy	301 TyrAs	snTyrLe	euSerThrAsp	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	uValCysProL	euHisAsnGln	320	Qy

GluValThrAlaGluAspGlyThrGluArgCysGluLysCysSerLysProCysAlaArg 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys GlyCysProAlaGluGlnArgAlaSerProLeuThrSer--------1,861

Oy 705 GlyMetValHisArgHisArg 712 	G ANTI-	; TITLE OF INVENTION: ANTIBODY MAXTANSINOID CONJUGATES; FILE REFERENCE: GENEUT. 03.42; FILE REFERENCE: GENEUT. 03.42; CURRENT APPLICATION NUMBER: 05.09/811,123; PRIOR APPLICATION NUMBER: 60/238,327; PRIOR APPLICATION NUMBER: 60/238,327; PRIOR FILING DATE: 2000-10-65; PRIOR FILING DATE: 2000-06-23; PRIOR FILING DATE: 2000-06-23): NOWBER OF SEQ ID NOS: 11 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 8 ; LENGTH: 3768 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-811-123-8	Alignment Scores: Pred. No.:	SEQ7 (1-712) x US-09-811-123-8 (1-3768) OY	Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40	Qy 41 ThrHisLeuaspMetLeuargHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60 	Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80	241 CAGGCTACGTCTCACAACCAAGTGAGGCAGGTCCCACTGCAGGGCGGGGGGGG	Oy 111111111111111111111111111111111111
ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	- 2 2	CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC	2341 TATGTCTCCGCCTTCTGGGCATCTGCCTGACATCCACGTGCACGTGGTGACACCAGCTT 2400 653	653 653 2461 GACCTGCTGAACTGGTGTATGCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520 653 653 2521 CTCGTACAGGGACTTGGCCGCTCGGAACGTGTCAAGAGTCCAACCATGTCAAA 2580	653 653 2581 ATTACAGACTTCGGGCTCGGCTGGTGGACATTGACGAGACAGAGTACCATGCAGAT 2640 653	2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2700 653	CACCAGAGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2761 AAACCTTACGATGGGATCCCAGCCCGGAGATCCCTGACCTGGTGGAAAAGGGGGAGCGG 2820 653	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTTGTAATTGTCGTGTCTGAAGTCCGGATGGCC	ASPSETTHT PHETYTATGGCCTTTGGGGTGGAATGGGGGGGGGGGGGGGGGG
da oy	o o o	8 6 6 6	6 6 6	oy de	oy ob	oy Oy	g &	8 6 8	δ DP	6

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1561 TGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620 541 ValGluGlucysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560 1621 GTGGAGCAATGCCGAGTACTGCAGGGGTCCCCAGGGAGTATGTGAATGCCAGGCACTGT 1680 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 1681 TTGCCGTGCCACCTGAGTCAGCCCAAATGCCTGTTTTGGACCGGAG 1740 581 AlaAspGlnCysValAlaCysAlaHisTyrLySASpProProPheCysValAlaArgCys 600 171111111111111111111111111111111111	601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620	ATCTGCTGGTCGTCGTCTTGGGGGTGGTTTTGGGATCCTCATCATCACGGGGGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100 653	653	653	653	653
9 9 9 9 9	OY OY Db	g da da d	8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Qy Db Qy Db	da Oy Oy	90 90 90 90	90 90 90 90 90
	3GCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCTGCCATGR 31yCysThrG1yProLysHisSerAspCysLeuAlaCysLeuHisPP 11	Oy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	321 GluvalThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 3	Db	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuDro 4	441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu	481 ProtrpaspGlnLeuPheargasnProHisGlnalaLeuLeuHisThralaasnP 481 ProtrpaspGlnLeuPheargasnProHisGlnalaLeuLeuHisThralaasnP 111111111111111111111111111111111111

41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAs 	31yTyrValLeu1leAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuAr 	301	CCCTGAACAATACCACCCCTGTCACAGGGCCTCCCCAGGAGGCCTGCGGGAGCT LeuargSerLeuThrGlu1leLeuLysGlyGlyValLeu1leGlnArgAsnProGl 	Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 18 	Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 2	Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	11aGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis ;	Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 28	Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300	Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 3	Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340	Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360	Qy 361 IleGlnGluPhealaGlyCysLysLysLlePheGlySerLeuAlaPheLeuProGluSer 38	Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 40 [11111111111111111111111111111111111
CACCAGAGTGATGTGGGAGTTATGGTGTGTGTGGGAGCTGATGACTTTTGGGGCC 2760	GGATG 28	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 2940	300	GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGTGCT 3060 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704 [SULT 3 -09-811-115-2 Sequence 2, Application US/09811115 Sequence 2, Application US/09811115 Setent No. US/2002003736A1 APPLICANT: Erickson, Sharon	APPLICANT: Schwall, Ralph APPLICANT: King, Kathleen TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL FILE REPERENCE: GENERAL 1034A	CURRENT FILING DATE: 2001-03-16 PRIOR APPLICATION NUMBER: 60/189,844	NOMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 2 LENGTH 3768	ORGANISM: Homo sapiens 9-811-115-2	0 Length: 3776.00 Matches: 67.94% Conservative:		(1-712) x US-09-811-115-2 (1-3768) 1 MetGluLeuhlaAlaLeuCysArgFrpGlyLeuLeuhlaLeuLeuProProGlyAla 20	rog1

Page 6

CORRENT FILING DATE: 2001-03-09 PRIOR APPLICATION NUMBER: US 09/493,480 PRIOR FILING DATE: 2000-01-28		653 653	Qy
FILE REFERENCE: U14UD8-UU98IUPC CURRENT APPLICATION NUMBER: US/09/854,		2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280	qa
APPLICANT: SmithKline Beecham Biologia TITLE OF INVENTION: HER-2/neu Fusion P		653 653 -	Qy
APPLICANT: Gheysen, Dirk APPLICANT: Corixa Corporation		2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	QQ
5	 	. 653	QY
Sequence 9, Application US/09854356 Patent No. US20020177567Al		2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGGAGCTG 2160	qa
	RES US-	653 653	QY
3121	QD	2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100	qq
GlyMetValHisHisArgHisArg	0у	653 653	Qy
3061 GAGGAGTATCTGGTACCCCAGCAGGGC	අ ග 	1981 ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGAGCAG 2040	QQ
	Qy	653 653	οy
3001 GACAGCATTTTACCGCTCACTGCTG	qa		q _Q
665 AspSerThrPheTyrArgSerLeuLeuC	Qy	GlvCvsProAlaGluGlnAraAlaSerProLeumhrser	· AO
2941 AGGGACCCCCAGCGCTTTGTGGTCATC	qq	021 GIYALACYSGIRPIOCYSPYOLIEASNCYSTRTHISSETCYSVALASPLeuAspAspLys 640	Š d
654	δŏ	CCCASCGGTGTGAAACCTGACCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	20
2881 ATTGACTCTGAATGTCGGCCAAGATTCC	G 40	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	oy 2
2821 CIGCCCCAGCCCCCATCIGCACCATIC	α 	1741 GCTGACCAGTGTGTGCCTGTGCCCACTATAAGGACCCTCCCT	qa
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2761 AAACCTTACGATGGGATCCCAGCCCGG	qa .		7 da
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2701 CACCAGAGTGATGTGTGGAGTTATGGTC	qa	Jai valeidelukyskiyvaliedelukiyikukiohityivalikinililililililililililililililililili	3 8
653	Qy	CCCAGIGIGICAACIGCAGCAGTICCTICGGGGCCAGGAGTGC	gr å
2641 GGGGCAAGGTGCCCATCAAGTGGATGC	g qq	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	Š Š
	Qy	GAGGACGACGAGGCCTGCCTGCCACCAGCTGTGCGCCCCGAGGCCACTGC	au .
2581 ATTACAGACTTCGGGCTGGCTCGCTG	qa	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	δo t
	Qy	CLUISSSALCASCILITIUSSAAUCUSCAUCUAAGIICIGUICCACUGGCCA	3 8
2521 CTCGTACACAGGGACTTGGCCGCTCGG	qa	481 ProtrpAspGinLeuPheArgAsnProHisGinAlaLeuLeuHisThrAlaAsnArgPro 500	Š Š
653	Oy	CIGGGCAGIGGACTCCICAICCACCATAACACCCACCICIGCIIGCACACGGIG	a (
2461 GACCTGCTGAACTGGTGTATGCAGATT	qa	461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrval 480 [VO E
653	^0	TACTCGCTGACCCT	ga
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OTHER INFORMATION: human HER-2/neu protein
NAME/KEY: misc_feature
LOCATION: (1). (1959)
OTHER INFORMATION: extracellular domain (EC
NAME/KEY: misc_feature
LOCATION: (2026). (3765)
OTHER INFORMATION: intracellular domain (IC
NAME/KEY: misc_feature
LOCATION: (2968). (3765)
OTHER INFORMATION: phosphorylation domain (IC
NAME/KEY: misc_feature
LOCATION: (2968). (3765)
OTHER INFORMATION: preferred portion of the
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PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 1999-01-29, NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 9 LENGTH: 3768
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ORGANISM: Homo sapiens
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Publication No. US20030157119A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
TITLE OF INVENTION: MATHOUS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.483C3
CURRENT APPLICATION NUMBER: US/10/313,644
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11111111111111111111111111111111111111	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684 111111111111111111111111111111111111	CludiuTyrLeuValProGinGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704			US-09-441-411-5 Sequence 5, Application US/09441411 ; Publication No. US20030008342A1	.RAL INFORMATION: LICANT: Scholler, Nathalle B.	LUCANT: DISIS, MAIY L. LICANT: Hellstrom, Ingegerd LICANT: Hellstrom, Karl Erik	AC:	RENI AFFILCALIUN NUMBER: US/US/441,411 RENT FILING DATE: 1999-11-16 BER OF SEO ID NOS: 26	SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 4473	TYPE: DNA ORGANISM: Homo sapiens -09-441-411-5		0 Length: 3776.00 Matches:	Best Local Similarity: 67.94% Mismatches: Ouery Match: 11.95.50% Indels: 336	daps: (1-4473)	1 Met	175 ATGGAGCTGGCGGCCTTGTGCCGCTGGGGGCTCCTCGCCCTCTTGCCCCCC	21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40			8			415 CAGGGCTACGTGCTCATCGCTCACAAGTGAGGCAGGTCCCCACTGCAGAGGCTGCGG 474	101 IleValargGlyThrGlnLeuPheGluAspAsnTyralaLeuAlaValLeuAspAsnGly 120	14	
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                                      oAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
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TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys ATTCTGCTGGTCGTGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGGATCCTGAAAGAGACGGAGCTG AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC -------q g δy Op δ g ò QQ oy do oy Db Qy Dρ δ q qq ò Ω g ò δ Q Q Qγ g Ω Q δy Q Ω g ò Q οχ

; APPLICANT: Old, Lloyd ; TITLE OF INVENTION: Breast Cancer Antigens ; FILE REFERENCE: LOO461/70130(JRV) ; CURRENT APPLICATION NUMBER: US/10/146,473 ; CURRENT FILING DATE: 2002-05-15 ; PRIOR PILICATION NUMBER: US 60/291,150 ; PRIOR FILING DATE: 2001-05-15 ; NUMBER: OF SEQ ID NOS: 82 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 32 LENGTH: 4473 ; TYPE: DNA CORGANISM: Homo Sapiens US-10-146-473-32	Alignment Scores: Pred. No.: Score: Score: Fercent Similarity: Best Local Similarity: Ouery Match: 14 SEQ7 (1-712) x US-10-146-473-32 (1-4473)	Oy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuLeuProProGlyAla 20	Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLySLeuArgLeuProAlaSerProGlu 40	Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60	Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnasp11eGlnGluVal 80	Oy 81 GlnGlyTyrValLeuTlealaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100	Oy 101 IlevalArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120		Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180	
Db 23995 CCTGGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2454 Qy 653	Qy 653	Db 2755 ATTACAGACTTCGGGCTGGCTGGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2814 Oy 653 653	2815	Db 2875 CACCAGAGTGATGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2934 Oy 653	Db 2935 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2994 Qy 653	Db 2995 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3054 Oy 653 653	Db 3055 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCGAATTCTCCCGCATGGCC 3114 Oy 654		Db 3235 GAGGAGTATCTGGTACCCAGGGGTTCTTCTGTCCAGACCCTGCCCGGGCGCTGGG 3294 Qy	RESULT 9 US-10-146-473-32 US-10-146-473-32 Sequence 3.2, Application US/10146473 Formarion No. US200301088881 GENERAL INFORMATION: APPLICANT: Scanlan, Matthew APPLICANT: Stockert, Ivan APPLICANT: Stockert, Elisabeth APPLICANT: Gure, Ali APPLICANT: Chen, Yao-Tseng

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SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
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 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTGTGAATTCTCCCGCATGGCC
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US-10-207-655-44

Sequence 44, Application US/10207655

Publication No. US2030118592A1

GENERAL INFORMATION.

APPLICANT: Ledbetter, Jeffrey A.

APPLICANT: Hayden-Ledbetter, Martha S.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOCLOBULIN FUSION PROFEINS

FILE REFERENCE: 3900-69, 401C1

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SECTION SEQ ID NOS: 426
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Matches:
Conservative:
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Db 151 ArggAgcrgGcG	2695 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2754	Dβ
Qy 1 MetGluLeuAla	653 653	Qy
SEQ7 (1-712) x US-09-877-1	2635 GACCTGCTGAACTGGTGTATGCAGTTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694	qa
	653 653	Qy
Percent Similarity: 67 Best Local Similarity: 67	2575 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2634	QQ
	653 653	Qy
Scores:	2515 TATGTCTCCGGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGGTT 2574	qq
; OKCANISM: HOMO SADIENS US-09-877-177-11	653 653	Qy
30	2455 CCCAAAGCCAACAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCCA 2514	qa
; SEQ ID NO 11	653 653	Οy
NUMBER OF SECTOR :	2395 CCTGATGGĞGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2454	qa
CURRENT PAPLICATION NUM	653 653	Qy
TITLE OF INVENTION: Met	2335 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2394	qa
APPLICANT: Peter V. Dar	653 653	Qy
; sequence 11, Application; publication No. US200201	2275 ACACCTAGGGGAGGGATGCCCAACCAGGGGGAGATGCGGATCCTGAAAGAGAGGGGGGTG 2334	qq
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DD 3295 GGCATGGTCCA	2215 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2274	QQ
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3175	2095 GGCTGCCCCGCCGAGAGAGAGAGCCCTCTGAGGTCATCTCTGCGGTGGTTGGC 2154	qa
665	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653	Qy
Db 3115 AGGACCCCAC		qa
Qy 654	621 GlyalaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640	δ
Db 3055 ATTGACTCTGAA	CCCAGGGGTGTAAACCTGACCTCCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGG	7 A
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Db 2995 CIGCCCAGCCC		. a
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Db 2815 GGGGCAAGGTC	1735 TGGGGGCCCACCCACCCACCCACCACCACCACCACCACCAC	3 A
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Qy	653					653
Ор	2815	GGGGGCAAG	GTGCCCATCAAG	TGGATGGCGCTGGAGTC	GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC	2874
Qy	653	1 1 1 1 1	1			653
qa	2875		GATGTGTGGAGT	TATGGTGTGACTGTGTG	CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTTGGGGGCC	2934
Qγ	653	1 1 1 1 1				653
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Qy	653	1 1 1 1 1 1	1			653
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ΟŸ	653	1			-1 -	653
qa	3055		GAATGTCGGCCA	AGATTCCGGGAGTTGGT	attgactctgaatgtcggccaagattccgggagttggtgtctgaattctccggcatggcc	3114
Qy	654			GlnAsnGluAs	-GlnAsnGluAspLeuGlyProAlaSerProLeu	664
Dp	3115	AGGGACCCC	CAGCGCTTTGTC	GTCATCCAGAATGAGGA	AGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	3174
Qy	999		PheTyrArgSer	LeuLeuGluAspAspAs	AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla	684
qq	3175	GACAGCACC	TTCTACCGCTCA	CTGCTGGAGGACGATGA	CATGGGGGACCTGGTGGATGCT	3234
Qy	685		LeuvalProGln 	GlnGlyPhePheCysPr 	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	3294
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δδ	3295	Glymetval 	GIYMETVALHISHISAFGHISAFG 	Arg /12 CGC 3318		
S · GPS · GPS · S	RESULT 11 US-09-877-17-11 US-09-877-17-11 Sequence 11, Application US, Sequence 11, Application US, GENERAL INFORMATION: APPLICANT PETER V. Danenbe, TITLE OF INVENTION: Rector FILE REFERENCE: 11220/13- CURRENT FILING DATE: 2001- CURRENT FILING DATE: 2001- CURRENT FILING DATE: 2001- CURRENT FILING DATE: 2001- SOFTWARE: FastSEG for Winde; SEQ ID NO 11 LENGTH: A530 TYPE: DNA ORGANISM: Homo sapiens US-09-877-177-11 Alignment Scores: Pred. No.: Score: Percent Similarity: 67.94% Best Local Similarity: 67.94% Best Local Similarity: 67.94% DB: SEQ7 (1-712) x US-09-877-177-1	7-177-11 7-177-11 7-177-11 7-177-11 INFORMATION: LINFORMATION: LOF INVENTION: FOR INVENTION: FOR INVENTION: FOR INVENTION: FOR INTERFERENCE: FOR INTERFERENC	ULT 11 09-877-177-11 cduence 11, Application US/09877177 cduence 11, Application US/09877177 cduence 11, Application US/09877177 cduence 11, Application US/09877177 cduence 11, Application US/0987177 cduence 11, Application US/09/67 cduence 12, Application Entry Eactor Receptor FILE OF INVENTION: Factor Receptor CURRENT APPLICATION NUMBER: US/09/67 cdurent FILING DATE: 2001-06-11 NUMBER OF SEQ ID NOS: 11 cduence 11 cduence 11 cduence 12 cduence 13 cduence 14	et al. determining Epidermal ceptor and HER2-New G /09/877,177 11 Version 4.0 Version 4.0 Matches: Conservative: Mismatches: Indels: Gaps: Indels: Gaps:	al Growth Gene Expression 4530 712 0 0 336	
Sy Bp Sy	1	MetGluLeu ATGGAGCTG	AlaAlaLeuCys 	ArgrrpGlyLeuLeuLe 	MetG1uLeuklaAlaLeuCysArgTrp61yLeuLeuklauklaLeuLeuBroProG1yAla 	20

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101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES FILE REFERENCE: 1546-R-00 CURRENT APPLICATION WUMBER: US/10/007,926A CURRENT FILING DATE: 2001-12-07 PRIOR PPLICATION WUMBER: 60/254,090 PRIOR FILING DATE: 2000-12-08 NUMBER OF SEQ ID NOS: 468 SOFFWARE: Patentin Ver. 2.1 SEQ ID NO 119 LENGTH: 4530
                                                                                                                                                                                                                                                                                                                                                                                    1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProFroGlyAla
                                                                                                                                                                                                                                                                                                                                                     LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
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Best Local Similarity:
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                                                                                             2491 TATGICICCCGCCTICTGGGCATCIGCCIGACATCCACGGTGCAGCIGGTGACACAGCIT 2550
                                                                                                                                         2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGCTCCCAG 2610
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                                                                                                                                                                                                                                                                                                                                                                                                                    2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG 2970
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                                                2431 CCCAAAGCCAACAAAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2490
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                                                                                                                                                                                                                                                                              2731 ATTACAGACTTCGGGCTGGCTGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTGAATTCTCCCGCATGGCC
                                                                                                                                                                                                           Sequence 119, Application US/10007926A
Publication No. US20030143539A1
GENERAL INFORMATION:
APPLICANT: BERTUCCT, FRANCOIS
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: VIENS, PATRICE
APPLICANT: VIENS, PATRICE
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221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240 [301 TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln	11 GAGGIGACAGCAGAGACAGAGAGAGAGAGAGAGAGAGAGA	81 PheaspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla		501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 111111111111111111111111111111111111	1 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHi 1 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHi 1 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

11eValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	1 alaGlyGlyCysAlaArgCysLySGlyProLeuProThrAspCySCysHisGluGlnCys 24	1 AGIGGCAICTGTGAGGTGCCCAGGCCCTGGTGACCTACAACACAGACAG	21 GluValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 34	CcAGGACTTGCTGCCAACAAGATCTTTGCGAGCCTGGCATTTCTAAGAGATTTGCTGCAATTTCTTGCTGCAATTTCTTGCAACACTTTGCTGCAACTTTTGCTGCAACTTTTTGCTGCAACTTGTTCTTTGCTGCAATTTCTTTGTTTTTGTTTTTTGTTTTTTTT
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Db 2971 CTGCCCCAGCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3030 Qy 653	AGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGTGGTGGTTCTACCGCTCGTGGTGGTGGTGTGTGT	US-10-101-510-124 Sequence 124, Application US/10101510 Publication No. US20030148295A1 GENERAL INFORMATION: APPLICANT: WANG, YIXIN TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE FILE REFERENCE: 15117.0012 CURRENT APPLICATION NUMBER: US/10/101,510 PRIOR APPLICATION NUMBER: 002-03-20 PRIOR APPLICATION NUMBER: 00276,947	15 Patent D NOS: 805 E: Patent D NOS: 805 O 124 DNA SM: Homo sapiens 510-124 Scores:	>	2 4 2 0 6 8 6 4 4

Db 2611 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG 2670 Qy 653	653	2851 CACCAGAGTGATGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGTTTGGGGCC	2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG	2971 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC	Oy 654	Oy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	Qy 685 GluGluTyrLeuValProGlnGlyPhePheCysProAspFroAlaProGlyAlaGly 704	705 GlyMetValHisHisArgHisArg 712	3271	RESULT 14 US-10-338-7-30-1	; Sequence 1, Application 05/10350/30; Publication No. US20030147905Al; General Information:	; APPLICANT: Genzyme Corporation ; APPLICANT: Nicolette, Charles A ; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS	; FILE REFERENCE: 5017C ; CURRENT APPLICATION NUMBER: US/10/338,730	; CURRENT FILING DATE: 2003-01-08 ; PRIOR APPLICATION NUMBER: US 09/527,487 . DELOW ETTING DAME: JACO-14	; FRIOR FILING DATE: 2002-03-10 ; NUMBER OF SEQ ID NOS: 10 : SOFTWARE: Patentin version 3.1	14530	; TYPE: DNA ; ORGANISM: Homo sapiens	; FEATURE: ; NAME/KEY: CDS	; LOCATION: (151)(3915) ; OTHER INFORMATION: US-10-338-730-1	Alignment Scores: Pred. No.: 0 Length: 4530
11111111111111111111111111111111111111	1651 GAGGACGAGTGTGGGGGGAGGGCTGGCCTGCCACCAGTGGGGGCCCCGAGGGCACTGC 1710 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540	541 ValGluGysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560 	561_LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 	601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620 	621 GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640 	GlycysproalagluglnargalaSerProLeuThrSer		2131 ATTCTGCTGGTCGTCGTCTTGGGGGTGCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2190 653 653	2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2250	653 653	51 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGAG	b53 653 2311 AGGAAGGTGAAGGTGCTTGGGGGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2370	653 653	2371 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2430	653 653	m	53	91 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT	653 653 2551 ATGCCTATGGCTGCTCTTAGACCATGTCGGGGAAAACCGGGGGACGCTGGGGTCCCAG 2610	

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IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys ATTCTGCTGGTCGTCGTCGTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGAGCAGCAG GlyCysProAlaGluGlnArgAlaSerProLeuThrSer-------

2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2250	. מוניים ל
653 653	25.
2251 ACACCTAGCGGAGCGATGCCCAACCAGGGGGCATGCGGATCCTGAAAGAGAGAG	; Publication No. US20030124128A1
653 653	; GENERAL INFORMATION: ; APPLICANT: Lillie, James
2311 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2370	: Glatt, Karen : Zhao, Xumei
653 653	; APPLICANT: Gandavarpu, Manjula ; APPLICANT: Kamatkar, Shubhangi
2371 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2430	
653 653	
2431 CCCAAAGCCAACAAAGAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2490	APPLICANT: APPLICANT:
653 653	APPLICANT: Meyers, Rachel E. APPLICANT: Bast Jr., Robert C.
2491 TATGICICCCGCCTTCIGGGCATCIGCCTGACATCCACGGTGCACCTGGTGACACAGCTT 2550	; APPLICANT: Hortobagy1, Gabriel N. ; APPLICANT: Pusztai, Lajos
653 653	
2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGGCTCCCAG 2610	Mills, Go
653 653	
2611 GACCTGCAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2670	
653 653	APPLICATION NUMBER: FILING DATE: 2001-00
2671 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2730	APPLICATION NUMBER: US FILING DATE: 2001-06-27
653 653	APPLICATION NUMBER: FILING DATE: 2001-07
2731 ATTACAGACTTCGGGCTGGCTGGCTGGCTGGACATTGACGAGAGAGA	APPLICATION NUMBER: FILING DATE: 2001-09
653 653	
2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2850	; PRIOR FILING DATE: 2002-05-14
653 653	; SOFTWARE: FastSEQ for Windows Version 4.0
2851 CACCAGAGTGATGTGGAGTTATGGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2910	; SEQ ID NO 125 ; LENGTH: 4530
653 653	; TYPE: DNA ; ORGANISM: Homo sapiens
2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCAAAAAGGGGGAGCGG 2970	0.5-1/1-01-30
653 653	No.: 0
2971 CTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3030	5/70.00 Matches: 67.94% Conservative:
653 653	r Local Similarity: 67.94% Mismatches: ry Match: 95.50% Indels:
3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 3090	
654	07 (1-712) x 1
3091 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCCAGCCAG	
665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	1.1
3151 GACAGCATCTTCTACCGCTCACTGCTGGACGATGGGGGGACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG	
685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704 	41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu
705 GlyMetValHisHisArgHisArg 712 	DD 2/1 ACCCACCTGGACAFGCTCCGCCACCTCTACCAGGGCTGCCAGGTGCTGCGGGAAACCTG 330 Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
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1 GAACTCACCTGCCCACCAATGCCAGCCTGTCCTTCCTGCAGGATATCCAGGAGGT 1 GINGlyTyTValLeuIlealaHisAsnGlnValArgGInValProLeuGlnArgLeuAr	CAGGGCTACGTGCTCATCGCTCACAACCAAG	1 IlevalargGlyThrClnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 	1 ASPProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 	GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGl:	CAGUITCGAAGCCICACAGAGAGTCTIGAAAGGAGGGGTCTIGAICCAGGGGAACCCC	<pre>1 beuCysiyicLhaspfintileLeuirpLysAspilePheHisLysAshashGinLeuAla </pre>	1 LeuThrLeulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCy		AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysH1sGluGlnC	GCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTG	1 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheasnHis 	1 SerGly11eCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	AGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGTCACCTACAACACAGACACGTTTGA	<pre>1 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro </pre>	1 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	-ပ္ပ	1 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCySSerLysProCysAlaArg	alCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrS	1 GTGTGCTATGGTCTGGGCATGGACCACTTGCGAGAGGTGAGGGCAGTTACCAGTGCCAAT	1 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 	lyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnVal			1 GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT	1 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	CCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGC
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1710 1830 1590 1650 1770 1950 2010 2070 2130 2190 2250 2370 2430 2310 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2550 460 480 500 520 540 260 580 009 620 640 653 653 653 653 653 653 2131 ATTCTGCTGGTCGTCGTCGTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2311 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2371 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 1 1 1 1 1 1 1 1 1 1531 1591 1651 1711 1771 1831 1891 1951 2011 2251 2431 2491 461 481 501 521 541 561 581 601 621 653 653 653 653 653 653 g Qy Db δy a δy QQ Ω DP QV Ωp Ω D QΥ g δ QQ ò Db Qγ qq QΥ QQ QΥ QQ QΥ ΩD δ QQ Ω Op Ω QQ ολ Q

οy	653 6	53	
QQ	2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2	2610	
οy	653 653	653	
qq	2611 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2	2670	
οy	653 6	653	
qq	2671 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2	2730	
Οy	9 653	653	
qq	2731 ATTACAGACTTCGGGCTGGCTGGCTGGTGGACATTGACGAGACAGAGTACCATGCAGAT 2	2790	
ογ	653 6	653	
qq	2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2	2850	
Οy	653 6	653	
qq	2851 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2	2910	
οy	653 6	653	
qq	2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGGAAAAGGGGGGAGCGG 2	2970	
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QQ	2971 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3	3030	
Oy	9	653	<i>:</i> -
qq	3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCGCATGGCC 3	3090	
Ολ	GlnAsnGluAspLeuGlyProAlaSerProLeu	664	
qa		3150	
Qγ		684	
qa	3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT 3	3210	
Qy	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 7	704	
qa		3270	
Οy	705 GlyMetValHisHisArgHisArg 712		
QQ	3271 GGCATGCTCCACCACGCACCGC 3294		
Search c	Search completed: October 17, 2003, 03:59:12	-	

Job time : 854.997 secs

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APPLICANT: Disis, Mary L.

TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGHANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
TITLE OF INVENTION: 4
CORRESPONDENCES: 4
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                         US-09-570-454-1

US-09-676-521-1

US-09-676-6108-25

US-08-621-356-1

US-09-676-6108-26

US-08-421-356-1

US-09-149-922-5

US-08-73-715-1

US-08-746-559A-3

US-08-746-559A-3

US-08-746-559A-3

US-08-746-559A-3

US-08-746-558-4
US-08-422-108-2
US-08-422-134-2
US-08-625-134-14
US-08-645-865-14
US-08-475-035-3
US-09-632-580A-3
US-09-632-580A-3
US-08-484-438-1
US-08-444-438-3
US-08-473-119-3
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US-09-668-822-9
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NAME: Sharkey, Richard G.
REGISTRAITON NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
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Patent No. 5869445
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APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
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      Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlp
-MODEL-frame+_p2n.model -DEV=xlp
-MODEL-frame+_p2n.model -DEV=xlp
-MODEL-frame+_p2n.model -DEV=xlp
-DE-fssued_patents_NA -OFWI=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
-MODE-LOCAL -OUTFMT-pto -NORM=ext -HBAPSIXES=500 -MINLEN=0 -MAXLEN=200000000
-USER=HOLLERANN80_CGN_1_1.403 @runat_15102003_131913_20570 -NCPU=6 -ICPU=3
-NO_MMAP -LANGEQUERY -NEG_SCORES=0 -MATLT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=10 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 1, Ap-
Sequence 2, A-
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Sequence 4, Ap-
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Sequence 3, Ap-
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                                                                                                                                                      October 15, 2003, 22:55:19; Search time 180.489 Seconds
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5: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-356-786-1
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US-08-229-515A-9
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US-09-167-322-4
US-09-167-322-4
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Maximum Match 100%
Listing first 45 summaries
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SEQUENCE CHARACTERISTICS
    LENGTH: 3768 base pai
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla
                                    GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
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APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
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OTHER INFORMATION: /note= "product = "cerB-b2""
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                       705 GlyMetValHisHisArgHisArg 712
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APPLICATION NUMBER: US/08/356,786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ7 (1-712) x US-08-356-786-1 (1-3768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               ; Sequence 1, Application US/08356786
; Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Pitcher, Edmund R. REGISTRATION NUMBER: 27,829 REFERENCE/DOCKET NUMBER: CRE TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT: Huston, James S. APPLICANT: Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: USA
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US-08-356-786-1
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Oy 361 IleGlnGluPheAlaGlyCysLysLysLlePheGlySerLeuAlaPheLeuProGluSer 380	Oy 401	Oy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440 -	Oy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480	Qy 481 ProTrpaspGlnLeuPheArgasnProHisGlnAlaLeuLeuHisThrAlaasnArgPro 5	Qy 501 GluAspGluCysValGlyGluGlyLeuAlacysHisGlnLeuCysAlaArgGlyHisCys 5	Qy 521 Db 1561	Qy 541 Db 1621	Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580	Oy 581 Db 1741	Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 6	Oy 621 GlyalaCysGlnProCysProIleAsnCysThrHisSerCysValAspLespAspLys 6	Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	QY 653	Qy 653	Db 2041 AAGATCCGGAAGTACACGATGCGGAGCTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	Oy 653
MetGluLeuAlaAlaLeuCysArgTrpClyLeuLeuLeuAlaLeuLeuProProGlyAla 20	caaccaccccaasierecaccaccaccacatafaasecrecagreccagreccagre hristeuaspmetteuarghisteuryrdinglycysginvalvaldinglyA 	rPheLeuGlnAspileGlnGluVal 8	nG1yTyrValLeulleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 10	ArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 	31yLeuArgGluLeu 1 	nProgln 1	nGlnLeuAla 1	ThrieulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 20 	SerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 	######################################	SLeuHisPheAsnHis 2 	eCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 2 		IySerCysThrLeuValCysProLeuHisAsnGln	raccitititaregadgiggarctgeaccegeregeer thralagiuasp61ythrGinargcysg1uLysCysSeriysProcys		ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360

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TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TITLE OF INVENTION: HUMAN HER-2 EXPRESSION NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA CITY: U.S.A. ZIP: 19103	OBLAN HEROMAS ESSNER	Alignment Scores: 0 Length: 4473 Pred. No.: 3776.00 Matches: 712 Score: 712 Percent Similarity: 67.94% Conservative: 0 Best Local Similarity: 67.94% Mismatches: 0 Query Match: 2 Gaps: 1 SEQ7 (1-712) x US-09-048-804-1 (1-4473)	Qy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20	Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60 1	81 GlnGlyTyrValLeurleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	Db 475 ATTGTGGGAGGCACCCAGCTCTTTGAGGACAATGCCCTGGCCGTGGTAGACAATGGA 534 Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuargGluLeu 140
Db 2161 AGGAAGGTGAAGGTGCTTGGACCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220 Qy 653	2281 CCCAAAGCCAACAAAGTTTTAGACGAAGCATACGTGATGGTGTGGGTCCCCA 653	Oy 653	Db 2821 CTGCCCCAGCCCCCATCACATCATGTCTACATGATCATGGTGGATG 2880 Qy 653	Db 2941 AGGGACCCCAGCGCTTTGTGGTCATCAGAATGAGGACTTGGGCCCAGCCAG		RESULT 3 US-09-048-804-1 Sequence 1, Application US/09048804 Fatent No. 5968748 Fatent INFORMATION: GENERAL INFORMATION: APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters

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uLysG] GAAAGC	leLeuTrpLysAspile	GAAGGA	TCGGGC	rGluAs	TGAGG	YProle	SSerAs	CTCTG	oAlaLe	AGCCC:	TACAT	ySerCy	ATCCTG	nArgCy	GCGGTG	SLeuAI CTTGCG	silePh	GATCTI	rAlaPr	TGCCCC	rLeuTy	CCTATA	nValIl	AGTAAT	yilese	CATCAG	SHisAs	OHisel	GGAACCCGCACCAAGCTC	a
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ThrGl 	Thril	ACGAT	ACCAA(GlyGl	GGAGA	ArgCy:	GlyPro	1111	LeuHis		GAGGG	ThrAs	ACGGA	Asp61	GATGG	GGCAT	Glycy	GGCTG	Alase	GCCTC	IleTh	ATCAC	GlnAsı	CAGAA	GlnGly	CAAGG	AlaLe	PheArc	TTTCG	GlyGl
SerLeu 	TyrGlnAspThrile	CAGGAC	ATAGAC	CysTrp	тестес	CysAla	CysThr	TGCACG	CysGlu	TOTORO	AATCC	LeuSer	CTTTCI	Alaglu	GCAGAG	OTTO GGTCTG	PheAla	TTTGCI	AspPro	GACCCA	GluGlu	GAAGAG	ValPhe	GTCTTC	LeuThrLeuGlnGlyLeu(ACCCTG	GlyLeu 	GlnIen	CAGCTCTTTCGG	Cysval
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seq7.rni

ValCysThrGlyThraspMetLysLeuargLeuProalaSerProGl GrGrGCaCcGGCaCaGaCaTGaaGCTGCGGCTCCCTGCCAGTCCCGA GrGrGCaCcGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGA MetLeuargHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLe 		141 GlnLeuargSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160	Qy 201 GlySerargCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220	261 SerGlylleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 2	Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	361 IleGlnGluPheAlaGlyCysLysllePheGlySerLeuAlaPheLeuProGluSer 38
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Fri Oct 17 07:48:15 2003

qq	1315 TTTGATGGGGACCCAGCCTCCAACACTGCCCGCTCCAGAGCAGCTGTTT 1374		
ΟΥ	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 4	Qy	653
Db		Ор	2455 CCCAAAGCCAACAAAGAA
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aa .	GACCTCAGEGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCC	Oy	653
y Q	441 TYSErLeuThr.LeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	qq	2575 ATGCCCTATGGCTGCCTC
δò	LeuGlySerGlyLeuAlaLeu1leHisHisAsnThrHisLeuCysPheValHisThrVal 48	QY	653
; <u>a</u>		QQ	33
Oy Pr	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 5	Qy Dp	653
a :	CULTISSEAUCASCIUTITUSSAAUCUSCAUCUSCIUTISCIUCACACUSCOA	οy	653
oy Op	501 GLUASPGLUCYSYAIGIYGLUGIYLEUALACYSHISGInLeuCysAlaArgGlyHisCys 520 	qq	2755 ATTACAGACTTCGGGCT
٥٨	TroglyProglyProThrglnCvsValAsnCvsSerGlnPheiemargGlvGlnGlnCvs 540	Qy	
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Qy	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560	δ	3
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yo 4	561 LeubrocyshisproGlucysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580	č, da	2935 AAACCTTACGATGGGAT
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qq	2275 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGGGGGTG 2334	; Sequen ; Patent	nce 9, Application US/08 No. 5518885
φy	653 653	; GENER ; APP	AAL INFORMATION: PLICANT: RAZIUDDIN
qq	2335 AGGAAGGIGAAGGIGCTIGGAICIGGCGCTITIGGCACAGICIACAAGGGCAICIGGAIC 2394	TIT	; APPLICANT: SARKAR, FAZLUL ; TITLE OF INVENTION: ERBB2
δ	653	TIT. ;	THE OF INVENTION: NEOF

QQ	2395 CCTGATGGGGAGA	GATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2454	4
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οy	653	653	53
QQ	2875 CACCAGAGTGATG	CACCAGAGTGATGTGTGGAGTTAATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2934	6
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οy	653	653	2
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qq	3055 ATTGACTCTGAAT	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCSCATGGCC 3114	
QY	654	GlnAsnGluAspLeuGlyProAlaSerProLeu 664	64
Dp	3115 AGGGACCCCCAGC	GCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	174
Qy	665 AspSerThrPheT	AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	8
qa	3175 GACAGCACCTTCT	ACCECTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGTGCT 3234	œ.
QY	685 GluGluTyrLeuV	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704	04
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٥y	705 GlyMetValHisHisArgHisArg	isArgHisArg 712	
qq	3295 GGCATGGTCCACC	ACAGGCACCGC 3318	
RESULTUS-08-08-08-08-08-08-08-08-08-08-08-08-08-	IS-08-229-515A-9 IS-08-229-515A-9 Sequence 9, Application US Patent No. 5518885 GENERAL INFORMATION: APPLICANT: RAZIUDDIN APPLICANT: SARRAR. FAX	US/08229515A AZI.II. H	
	FITLE OF INVENTION: E	ERBB2 PROMOTER BINDING PROTEIN IN NEOPLASTIC DISEASE	

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LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
                                                       GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
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                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELEPHONE: 404-688-9980
      SENBERG PC
Street, Suite 1200
                                                                                                                                                                                                                                                                                   (1-712) x US-08-229-515A-9 (1-4530)
       ROSENBERG
                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        3776.00
67.94%
67.94%
95.50%
      ADDRESSEE: NEEDLE & ROSI
STREET: 127 Peachtree Si
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
                                                                                                                                                                                LENGTH: 4530 base pairs
                                                                                                                                                                                       ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-9
                                               COMPUTER READABLE FORM MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 653	Oy 653	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGjyAlaGly	RESULT 6 US-08-645-865-9 Sequence 9, Application US/08645865 Patent No. 5654406 GENERAL INFORMATION: APPLICANT: RAZIUDIN APPLICANT: SARKAR, FAZLUL H TITLE OF INVENTION: RRBB2 PROMOTER BINDING PROTEIN IN TITLE OF INVENTION: NEOPLASTIC DISEASE	NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: STREET: 127 Peachtree Street, Suite 1200 CITY: Atlanta STRETE: Georgia COUNTRY: usa 2 IP: 30303 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: Descart	, 865 , 865
	We consider the construction of the construc	GGCTGCCCGCCGAGAGAGAGCCAGCCTCTGACGTCCATCGTCTCTGGGGGTGGTTGGC		y 653 2371 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2430 y 653	1 ATTACAGACTTCGGGCTGCTGGGAAAACCGGGACGCCTGGGCTCCCAG 3

	3.1 GluvalThraaGluaspGlYThrGlangCySGluLySCySsElyStroCysalaarg 340		IleGlnGluPheAlaGlyCysLysLjePheGlySerLeuAlaPheLeuProGluSer 	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400 	401 GluthrLeuGluGluIlethrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420 	421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440 	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460 	461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480 	481 ProTrpaspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	501 GluaspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560 	561 LeuproCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620 	621 GlyalaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640 	641 GlycysProAlaGluGlnArgAlaSerProLeuThrSer	653 653
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7	ed. No.: 07.00 Length: 433 ore: 3776.00 Matches: 712 ore: 712 crent Similarity: 67.94% Conservative: 0 st Local Similarity: 67.94% Mismatches: 0 ery Match: 95.50% Indels: 336	Gaps: 1 55-9 (1-4530)	Qy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla 20	Oy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40	41 ThrHisLeuAspWetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60	61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspileGlnGluVal 80 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	8 GlnGlyTyrValLeulleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 10	01 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 	121 AsproLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArg(1 1 1 1 1 1 1 1 1	141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 16	161 LeuCysTyrGlnAspThrileLeuTrpLysAspilePheHisLysAsnAsnGlnLeuAla 1 11 11 11 11 11 11 11	LeuThrLeulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 20 	201 GlyserArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 22	221 AlaciyciysAlaArgCysLysciyProLeuProThrAspCysCysHisGluGinCys 24	241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 26	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 28 [281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 30	GT

Qy 705 GlyMetValHisHisArgHisArg 712	Db 3271 GGCATGGTCCACAGGCACCGC 3294		; Sequence 4, Application US/09167322 ; Patent No. 6365151	: egheny Universit	Sciences, England,	; TITLE OF INVENTION: CANCER VACCINE ; NUMBER OF SEQUENCES: 14	(2)		STATE: PA COUNTRY: USA		MEDIUM TIPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATIB	SOFTWARE: PatentIn Release #1.0	CORRENT APPLICATION NUMBER: US/09/167,3	FILING DATE: U/-000-1998	; PALOK APPLICATION DATA: ; APPLICATION NUMBER: PCT/US97/00	FILING DATE: <unknown> HTTORNEY/AGENT INFORMATION:</unknown>		TELECOMMUNICATION INFORMATION:	8-838 5549	. : :		STRANDEDNESS: single TOPOLOGY: linear	; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-167-322-4	nent Scores:	3776.00	11arity: b/.94% Conse Similarity: 67.94% Misma		SEQ7 (1-712) x US-09-167-322-4 (1-4530)	Qy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyI	Db 151 ATGGAGCTGGCGGCCTTGTGCCGCTGGGGGG	Qy 21 AlaSerThrGlnValCysThrGlyThrAspM	Db 211 GCGAGCACCCAAGTGTGCGCCACGGCACAGACA	Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrC	Db 271 ACCACCTGGACATGCTCGGCCACTCTACC Ov 61 GluLeuThrTvTLeuProThrAsnAlaSerI	
1 ATTCTGCTGGTCGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAAAACGGAAACGGAGCTGTGGAGCCGCTG 2250	653 653	2251 ACACCTAGCGGAGGGATGCCCAACCAGGCGCAGATGCGGAATCCTGAAAGAGAGGGGGGGTG 2310	653 653	2311 AGGAAGGTGAAGGTGCTTGGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2370	653 653	2371 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2430	653 653	2431 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2490	653 653	2491 TATGTCTCCGGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACAC	653 653	2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGGCTCCCAG 2610	653 653	2611 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2670	653 653	2671 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2730	653 653	2731 ATTACAGACTTCGGGCTGGCTGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2790	653 653	2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2850	653 653	2851 CACCAGAGTGATGTGTGGGGTTATGGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2910	653 653	2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2970	653 653	2971 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATGTCAAAATGTTGGATG 3030	653 653	3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTAATTCTCCCGCATGGCC 3090	654	3091 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684		685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704 11	
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ThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80 REALMBLE FORM
TYPE: FLOPPY disk
PUTER: IBM PC compatible
RATING SYSTEM: PC-DOS/MS-DOS
TWARE: Patentin Release #1.0, Version #1.30
TWARE: Patentin Release #1.0, Version #1.30
TIGATION NUMBER: US/09/167,322
SIECRTICATION DATA:
LICATION NUMBER: US/09/167,322
ING DATA:
LICATION NUMBER: PCT/US97/00582
ING DATA:
LICATION NUMBER: PCT/US97/00582
ING DATA:
CE: Monaco, Daniel A.
ISSTRATION NUMBER: 7933-33 PC
UNICATION NUMBER: 7933-33 PC
UNICATION INFORMATION:
E: MONACO, DANIEL A.
UNICATION INFORMATION:
CHARACTERISTICS:
CHARACTERISTICS: NCE ADDRESS: SEE: Seidel, Gonda, Lavorgna & Monaco, P.C. : Suite 1800, Two Penn Center Plaza Philadelphia 4530 712 0 0 336 1 Allegheny University of the Health Sciences, Halpern, Michael S. England, James M. WYENTION: CANCER VACCINE Length:
Matches:
Conservative:
Mismatches:
Indels: H: 4530 base pairs nucleic acid DEDMESS: single OGY: linear ESCRIPTION: SEQ ID NO: 4: -167-322-4 (1-4530) ation US/09167322 YY: USA 19102 SADABLE FORM: 0 3776.00 67.94% ty: 67.94%

Page 13

Db 1411 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCC 1	0.y 441 TYPSELBUTATIONSINGLYLEUGIYLESETTPLEUGIYLEUGIYLEUGIGUU 4 100 Db 1471 TACTCGCTGCAAGGCTGGGCATCAGCTGGGGGTGGGGCTGGGGTTGGCTGCGGGTGGGGAA 1 3 450	AlaLeuAlaValLeuAspAsnGly 120 461 LeuGlySerGlyLeuAlaLeuAlaValLeuAspAsnGly 120 461 LeuGlySerGlyLeuAlaValLeuAspAsnGly 120 461 LeuGlySerGlyLeuAlaValLeuAspAsnGly 120 461 LeuGlySerGlyLeuAlaValLeuAspAsnGly 120 461 LeuGlySerGlyLeuAlaCalaCalaCalaCalaCalaCalaCalaCalaCalaC	luteu 14	rogin 16	uAla 18	SLYS 20	alCys 22 	lnCys 24	26	, 0	sPro 30	nGln 320	laArg 3 	laAsn 360	Sericaded and Taccada	Phe 400	420	440
	81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuAr 	101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAs 																

Oy 301 TyrAsnTyrLeuSer'	MAMEATICUS 1. LOCATION: (151)(3915) US-09-527-487-1
991	ORGANISM: Homo sapiens FEATURE NAMPYREV: CHG
Qy 281 SerMetProAsnProC	; LENGTH: 4530 ; TYPE: DNA
931	SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1 TENGRI: ACSO.
Qy 261 SerGlyIleCysGlul	CURRENT FILING DATE: 2000-03-16 ; NUMBER OS SEQ ID NOS: 9
Db 871 GCTGCCGGCTGCACGC	CURRENT APPLICATION NUMBER: US/09/527,487
Qy 241 AlaAlaGlyCysThro	TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES FILE REFERENCE: 126881309200
Db 811 GCGGTGGCTGTGCC	GENERAL INFORMATION: APPLICANT: Nicolette, Charles
Qy 221 AlaGlyGlyCysAlaA	Sequence 1, Application US/09527487 Patent No. 6528060
Db 751 GGCTCCGCTGCTGG	RESULT 8 US-09-527-487-1
Qy 201 GlySerArgCysT	Db 3271 GGCATGGTCCACCACACGCACCGC 3294
Db 691 CTCACACTGATAGAC	Oy 705 GlyMetValHisHisArgHisArg 712
Oy 181 LeuThrLeuIleAsp	Db 3211 GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTGTCTGTCCAGACCCTGCCCCGGGCGCTGGG 3270
Db 631 CTCTGCTACCAGG	Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704"
Qy 161 LeuCysTyrGlnAsp?	Db 3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT 3210
Db 571 CAGCTTCGAAGCC	Oy 665 AspSerThrPheTyrArgSerLeuCluAspAspAspAspMetGlyAspLeuValAspAla 684
Qy 141 GlnLeuArgSerLeu?	Db 3091 AGGGACCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG
Db 511 GACCCGCTGAACAAT	Oy 654
Qy 121 AspProLeuAsnAsn?	Db 3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCGCATGGCC 3090
Db 451 ATTGTGCGAGGCACC	Qy 653 653
Qy 101 IlevalArgGlyThr	Db 2971 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3030
Db 391 CAGGGCTACGTGCTC	Qy 653 653
Qy 81 GlnGlyTyrValLeu	Db 2911 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGGAAAAGGGGGGAGCGG 2970
Db 331 GAACTCACCTACCTG	Qy 653 653
Qy 61 GluLeuThrTyrLeul	Db 2851 CACCAGAGTGATGTGGAGTTATGGTGTGAGTGTGTGGGGGCTGATGACTTTTGGGGCC 2910
Db 271 ACCCACCTGGACATG	Qy 653 653
Qy 41 ThrHisLeuAspMet	Db 2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2850
Db 211 GCGAGCACCCAAGTG	Qy 653 653
Qy 21 AlaserThrGlnVald	Db 2731 ATTACAGACTTCGGGCTGGCTGGCTGGTGGACATTGACGAGACAGAGTACCATGCAGAT 2790
Db 151 ATGGAGCTGGCGCC	Qy 653 653
Qy 1 MetGluLeuAlaAla1	Db 2671 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2730
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Best Local Similarity: 67.94	Qy 653 653
NO.:	Db 2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2610
Scores:	EG9 500 AO

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336
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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13.1 TACAACTACCTTICTACGGACGTGGGATCCTGCACCTCGCCCCTGCACACACA		UY 033	653	2251 ACACCCCACCCCACCCCACCCCACCCCACCCCACCCC	4231 ACACCINGCGGAGGGAGGGGGGGGGGGGGGGGGGGGGGGG	UY 033	653	2371 CTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC	653	Db 2431 CCCAAAGCCAACAAAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2490	Ογ 653 ······ 653	Db 2491 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2550	Qy 653 653	Db 2551 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGGACGCCTGGGCTCCCAG 2610	Qy 653 653	Db 2611 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2670	ζγ 653 653	Db 2671 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2730	Qy 653 653	Db 2731 ATTACAGACTTCGGGCTGGCTGGCTGGTGGACATTGACGAGACAGAGTACCATGCAGAT 2790	Qy , 653 653	Db 2791 GGGGGCAAGGTGCCCATCAAGTGGATGGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2850	Ογ 653 653	Db 2851 CACCAGAGTGATGTGGAGTTATGGTGTGACTGTGGGAGCTGATGACTTTTGGGGCC 2910	0у 653 653	Db 2911 AAACCTTACGATGGGATCCCAGCCGGGAGATCCCTGACCTGGTGGAAAAGGGGGGAGCGG 2970	Ογ 653 653	Db 2971 CIGCCCCAGCCCCCATCIGCACCATIGAIGTCIACAIGAICAIGGICAAAIGIIGGAIG 3030	Qy 653 653	Db. 3031 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCGCATGGCC 3090	654GlnAsnGluAspLeuGlyProAlaSerProLeu	3091 AGGGCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCCAGCCCTTG	Vy bob sabserintraperyratyserieureutusapasbaspmeetujaspetaa b84		
<u> </u>	1 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCCCTGCACAACAA	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	GAGGTGACAGCAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA	1 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	1 GTGTGCTATGGTCTGGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGTGCCAAT	1 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	1 ATCCAGGAGTTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCGGAGAGC	1 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	TTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	I GAGACICIGGGAGGATCACAGGTTACCTATACATCTCAGCATGGCCCGGACAGCCTGCCT	Aspirence: valries.iiasiinelusiivalliearigsiyargilelelilisasiio.jyala 	######################################	1 17 17 17 17 17 17 17 17	1 LeuGlySerGlyLeuAlaLeuIleHisHisHisAsnThrHisLeuCysPheValHisThrVal		ProTrpAspGlnLeuPheArqAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro		GluðspGluCvsValGlvGluGlvLeuAlaCvsHisGluLeuCvsAlaardGlvHisCvs	CASCACCACTGTCTGGGCGAGGCCTGGCCTGCCACCACTGTCTGT	TrpGlvProGlvProThrGlnCvsValAsnCvsSerGlnPheLeuArgGlvGlnGluCvs		ValGluGluCysArqValLeuGlnGlvLeuProArqGluTyrValAsnAlaArqHisCys		LeuproCvsHisProGluCvsGlnProGlnAsnGlvSerValThrCvsPheGlvProGlu		AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArqCys		ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu		GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys	GGGGCATGCCAGCCTTGCCCCATCAACTGCACCCACTGTGTGTG	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	GGCTGCCCCGCCGAGCAGAGCCAGCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC	3

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                                                                                                                                                                         APPLICANT: K. Danenberg
APPLICANT: K. Danenberg
TITLE OF INVENTION: Method of determining Epidermal Growth
TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
FILE REPERENCE: 11220/120
CURRENT PILITIO DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 4530
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GlyMetValHisHisArgHisArg
                       GGCATGGTCCACCACAGGCACCGC
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Patent No. 6582919
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: HOMC
US-09-877-177A-11
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Length: Matches: Conservative: Mismatches: Indels: Gaps:	385)	yteuteu 	cecreeeeecrecreeree	AlaSerThrGlnValCysThrGlyThrAspWetLysLeuArgLeuProAlaSerPrv 	HisLenTure noglavos	CACCTCTACCAGGGCTGCC	AsnAlaSerLeuSerPhel	AATGCCAGCCTGTCCTTCC	GInGlyTyrValLeuIleAlaHisAsnGInValArgGlnValProLeuGlnArgLei 	CACAACCAAGTGAGGCAGG	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaVa	TTTGAGGACAACTATGCCC	AspProLeuAsnAsnThrTroValThrGlyAlaSerProGlyGlyLeuArgGlu:	cerercacaegecerece	GInLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGInA.	ATCTTGAAAGGAGGGGTCT	rIleLeuTrpLysAspIlePheH	TTGTGGAAGGACATCTTCC	rgSerArgAlaCysHis	screressecriseers	rGluAspCysGln	TGAGGATTGTCAG	sLysGlyProLeuProThrAspCys(sHisSerAspCy	SCACTCTGACTGCCTG	CysProAlaLeuValThrTyrAsnThrAspThr	TGCCCAGCCCTGGTCACCT	erMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAl	CGGTATACATTCGGCGCCA	ValGlySerCysThrLeuV
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lignment Scorred. No.: core. core. sercent Simila. est Local Sim. uery Match: B:	(1-712)		11	21	41	131	61	191	81	251	101	311	121	371	141	431	161	491	181	551	201	+ 1	221	241	731	261	791	281	851	301
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                                                GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Composition and Method
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
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Matches:
Conservative:
Mismatches:
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                        Sequence 3, Application US/08579823A Patent No. 6080409
                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: JUGGe, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET UNMBER: 7636
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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3632.00
98.65%
98.65%
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SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
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INDIVIDUAL ISOLATE: GM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
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Best Local Similarity:
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TYPE: nucleic
STRANDEDNESS:
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RESULT 11
US-08-579-823A-3
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ORIGINAL SOU
                                                                                                                                                                        CITY: Pa.
STATE: C.
COUNTRY:
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                                              GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys
                                                                                                                        TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys
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                                                                                                                                                             GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruegg, Curtis L.
Wu, Hongyu
OF INVENTION: Immunostimulatory Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                   1982 GCCGCTCGCCCAGCCCAGCACA 2005
                                                                                                                                                                                                                                                                                                                                                                                                                   661 Ala---SerProLeuAspSerThr 667
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CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Asso
STREET: 350 Cambridge Ave.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09344195
Patent No. 6210662
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Laus, Reiner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-344-195-3
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LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
                                                              NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
<Unknown>
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                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
N FOR SEQ ID NO: 3:
                                                                                                                                                        NCE CHARACTERISTICS:
LENGTH: 2385 base pairs
                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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98.65%
98.65%
91.86%
CLASSIFICATION:
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Best Local Similarity:
                                                                                                                                          INFORMATION FOR
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APPLICANT: Hudziak, Robert M.
APPLICANT: Shepard, H. michael,
APPLICANT: Ulrich, Axel
TITLE OF INVENTION: HER2 EXTRACELLULAR DON
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       667
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,108
FILING DATE: 14-Apr-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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3R: 554C2D2
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APPLICATION NUMBER: 08/048346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 1982 GCCGCTCGCCCAGCCCCAGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/355460 FILING DATE: 13-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                              TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln
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STRANDEDNH TOPOLOGY: S-08-422-108-2	EDNESS: S SY: Linea:	ingle r			
Alignment Score Pred. No.: Score: Percent Similar Pert Local Sim. Query Match:	res: arity: nilarity:	1.77e-299 3471.00 99.84% 87.78%	Length: Matches: Conservative: Mismatches: Indels:	1872 623 0 0 0 0	
v (1-712) v	x US-08-42	2-108-2 (1-18	72)		
22	SerThrGln'	ValCysThrGlyTh 	rraspMetLysLeuArg 	SerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGluThr 	41
42	HisLeuAsp CACCUGGAC	MetLeuargHisLe 	euTyrGlnGlyCysGlnV	HisteuaspmetteuargHisteuTyrGlnGlyCysGlnVàlValGlnGlyasnteuGlu LHIIIIIIIIIIIIIIIIIIIIIIII CACCUGGACUGGICCGCCACCICTACCAGGGGTGCTGCAGGTGGTGCAAACTGGAA	120
62	LeuThrTyr CUCACCUAC	thrTyrLeuProThrAsnAl	aSerLeuSerPheLeu(OThrasnalaSerLeuSerPheLeuGlnaspileGlnGluValGln 	. ⊢ œ
82	32 - 52	LeullealaHisas 	snGlnValArgGlnValI 	gil 	
102	ValArgGly GUGCGAGGC	ThrGlnLeuPheGl	LuAspAsnTyrAlaLeu 	A – S	121
122	ProLeuAsn 	AsnThrThrProve	alThrGlyAlaSerProc 	oLeuasnasnthrThrProValThrGlyAlaSerProGlyGlyLeudgGluLeuGln 	141 360 `
142	LeuArgSer 	LeuThrGlulleLe 	euArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnAr 	IleglnArgAsnProglnLeu 	161 420
162	CysTyrGln UGCUACCAG	AspThrIleLeuTr 	rpLysAspIlePheHisI 	STyrGlnAspThrileLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeu 	181
182	Thr	AspThrAsnArgSe 	erArgAlaCysHisProC 	LeulleaspThrasnargSerargalaCysHisProCysSerProMetCysLysGly 	201
202	SerArgCys'	TrpGlyGluSerSe UGGGGAGAGAGUUC	arGluAspCysGlnSerl UGAGGAUUGUCAGAGCC	erArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCysAla 	221
222	GlyGlyCys. GGUGGCUGU	AlaArgCysLysGl 	LyProLeuProThrAspC 	GlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCysAla 	241
242	Alaglycys' GCCGGCUGC	ThrGlyProLysHi 	AlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCy. 	SysteutisPheasntisSer 	261
262	GlyileCys GGCAUCUGU	GlyIleCysGluLeuHisCysProAlaLeuVa 	roalaLeuValThrTyr/ 	ThrTyrasnThraspThrPheGluSer 	281.
282	MetProAsn 	ProGluGlyArgTy 	oAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAli 	?ysValThrAlaCysProTyr 	301 840
302	AsnTyrLeu: 	SerThraspvalg] 	AsnTyrLeuSerThraspValGlySerCysThrLeuValCy 	CysProLeuHisAsnGlnGlu 	321 900

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                        CysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsnIle
       GlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPhe
                                                                                                    ValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArgVal
                                                        AspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPheGlu
                                                                                                                                   GlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrValPro
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Matches:
Conservative:
Mismatches:
Indels:
                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
       APPLICANT: Hudziak, Robert M.
APPLICANT: Shepard, H. Michael
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HER2 EXTRACELLULAR INUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 CURKERT AFPLICATION DATA:
APPLICATION NUMBER: US/08/422,734
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422108
FILING DATE: 14-APF-1995
APPLICATION NUMBER: 08/355460
FILING DATE: 13-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/48346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/354319
FILING DATE: 19-APR-1989
ATTORNEY APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
ATTORNEY AFFERT INFORMATION:
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TELECOMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELERA: 415/35-981
TELERA: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                       NAME: Lee, Wendy M
REGISTRATION NUMBER: 00,000
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542	2 GluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCysLeu 561
562	12 ProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAla 581
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1741	12 SerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGluGluGly 621
622	2 AlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLysGly 641
64; 186	.2 CysProAlaGlu 645 1 UCCCCGCCGAG 1872
SSULT 15 Sequence 14 Sequence 14 Sequence 14 Sequence 14 APPLICAN TITLE OF	RESULT 15 US-08-229-515A-14 US-08-229-515A-14 US-08-229-515A-14 US-08-229-515A-14 Sequence 14. Application US/08229515A Sequence 14. Application US/08229515A Sequence 14. Application US/08229515A SEQUENCE 14. Application US/08229515A TITLE OF INVENTION: REBB2 PROWOTER BINDING PROTEIN IN TITLE OF INVENTION: REDPLASTIC DISEASE NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS: ADDRESSEE: NEEDLE 6 ROSENBERG PC STREET: 127 Peachtree Street, Suite 1200 STRAFE: Georgia COUNTRY: USA STATE: Georgia COMPUTER: ISA SOFTWARE: PLOPPY disk MEDIUM TYPE: Floppy disk COMPUTER: ISA SOFTWARE: Patentin Release #1.0, Version #1.30 COMPUTER: 19 APR 1994 STLING DATE: 19 APR 1994 CLASSIFICATION NUMBER: 33,438 REGISTRATION NUMBER: 33,438 REGISTRATION NUMBER: 33,438 REGISTRATION NUMBER: 1414.608 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:

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    ; INFORMATION FOR SEQ ID NO: 14.; SEQUENCE CHARACPERISTICS:
; LENGTH: 3955 base pairs; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Best Local Similarity:
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	GluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAsp	δ d	653SerGlnAsnGluAspLeuGlyProAlaSer 662
_	1886 GAGGAGGGCATATGCCAGCCGTGCCCCATCAACTGCACCCCACTCCTGTGTGGGATCTGGAT 1945	_	

QY	663	663 ProLeuAspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuVal 682
qq	3026	CCCATGGACAGTACCTTCTACCGTTCACTGCTGGAAGATGATGACATGGGTGACCTGGTA 3085
ογ	683	683 AspAlaGluGluTyrLeuValProGlnGlyPhePheCysProAspProAlaProGly 702
qq	3086	3086 GACGCTGAAGAGTATCTGGTGCCCCAGGGATTCTTCTCCCCGGACCCTACCCCAGGG 3145
Qy	703	703 AlaciyGlyMetValHisHisArgHisArg 712
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and is derived by analysis of the total score distribution
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-LOOPEXT-0 -UNITS-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -TRREMIN=0 -ALIGN=15
-WODE-LOCAL.OUTEMT-pcto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN=200000000
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1140 1080 1260 1320 1200 440 480 360 380 420 460 160 180 200 900 220 999 240 260 840 320 960 400 720 780 280 300 900 LeuCysTyrClnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla CTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCT GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 1021 1081 1141 401 1201 1261 1321 1381 121 361 141 421 161 481 181 201 601 221 661 241 721 261 781 281 301 901 321 961 341 361 381 421 441 461 g οy g οy Db δ g οy П Qγ Ω Qγ Db ò qq Qγ qq Ω q δ Q δ qq Qγ g δy g Qγ Dp δ QQ ò Ob Ω q

2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA	Qy 653	Ογ 653 653	2641 GGGGCAAGGTGCCCATCAAGTGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC	Oy 653 653 Db 2701 CACCAGAGTGATGTGTGAGTTATGGTGACTGTGGGGAGCTGATGATTGGGGCC 2760	ογ 653 653	2761 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG	Qy 653 653 Db 2821 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 2880	0y 653 653 Db 2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGCC 2940	Oy 654	Oy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	DD 3061 GAGGAGTATCTGGTACCCCAGGAGGTTCTTCTGTCCAGACCCTGCCCGGGCGCTGGG 3120 Oy 705 GlymetvalHisHisArqHisArq 712	3121 GGCATGGTCCACCACAGGCACCGC	RESULT 2 AATA0739	ID AAT40739 standard; cDNA; 3768 BP.	AAT40739;	DT 01-JAN-1997 (first entry) DR HEB-2/Agii oncorded		KW breast cancer; ovary cancer; colon cancer; lung cancer; WW prostate cancer; genetic immunisation; tumour; vaccine; vector;	XX XX OS Homo sapiens.	Кеу	CDS 13765 /*tag= b		AA WO9630514-A1.	AA PD 03-OCT-1996. XX	FF 28-MAR-1996; 96WO-US01689. XX	PR 31-MAR-1995; 95US-0414417.
481 ProfrpaspGlnLeuPheArgasnProHisGlnalaLeuLeuHisThralaasnArgPro 500	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	1991 Gradoncanatatatagaccanadaccitaccitaccaccaccaccaccaccaccaccaccaccaccaccacc	1561 TGGGGTCCAGGGCCCAGTGTGTGTTTTTTTTTTTTTTTT	541 ValGluGluCysArgValLeuGluGlyLeubroArgGluTyrValAsnAlaArgHisCys	1621 GIEGGAGGAATGCCGAGTACTGCAGGGGTCCCCCAGGGAGTATGTGAATGCCAGGCACTGT	551 LeuprocystalsproditucysGinprodinasnGlySerValthroysDheGlyProGlu 580	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	601 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 	621 GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	1921	198	653	653	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG	653 653	2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	653	2221 CCTGATGGGAGAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280	2281 CCCAAAGCCAACAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	653 653	2341 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACGTT 2400	653 653	2401 AIGCCCTAIGGCIGCCICTIAGACCAIGICCGGGAAAACCGCGGACGCCTGGGCICCCAG 2460	653 653	2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520	653 653
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                                                                                                                                       Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-erbB2) protein (AAW01111). The oncogene is overexpressed in various cancers, including breast, overlan, colon, lung and prostate, and appears to induce malignancies through quantitative mechanisms that result from increased or dergulated expression of an essentially normal gene product. Nucleotides 2026-3765 of the cDNA sequence code for the intracellular domain (Lys676-vall255) of the HER-2/neu protein, which is useful for immunisation against malignancy. Nucleic acids can be used to direct expression of the intracellular domain in transformed host cells, or are used, alone or in a viral
                                                                                                                                                                                                                                                                                                                                                                                      IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                               LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMétCysLys
                     GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
                          TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisAsnGln
                                                                                                                                                  GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg
                                                                                                                                                                       ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn
                                                                                                                                                                                                                                                                                                                         ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro
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   immune response
for treating or
eliciting an
particularly
             an HER-2/neu associated malignancy, preventing tumours
polypeptides - for
 HER-2/neu
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Claim la; Column 23-32; 26pp; English

This sequence encodes the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.

other Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0

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Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	<pre>cores: ilarity: Similarity: :</pre>	1.04e-235 3776.00 67.948 67.948 95.508	Length: Matches: Conservative: Mismatches: Indels: Gaps:	3768 712 0 0 336	
SEQ7 (1-712	x AAX01912	(1-3768)			
Qy	1 MetGluLeu	AlaAlaLeuCysArg	TrpGlyLeuLeuLeuA	laLeuLeuProProGlyAla	20
qq	1 ATGGAGCTG	GCGGCCTTGTGCCGC	TGGGGCTCCTCCTCG	ATGGAGCTGGCGGCCTTGTGCCGCTGGGGGCTCCTCGCCTCTTGCCCCCC	09
δy	21 AlaSerThr	GlnValCysThrGly	ThrAspMetLysLeuA	rgLeuProAlaSerProGlu	40
qa	61 GCGAGCACC	CAAGTGTGCACCGGC	ACAGACATGAAGCTGC	GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG	120
٥y	41 ThrHisLeu	AspMetLeuArgHis	LeuTyrGlnGlyCysG	InvalvalGlnGlyAsnLeu	09
Db 1	21 ACCCACCTG	GACATGCTCCGCCAC	CTCTACCAGGGCTGCC	ACCCACCTGGACATGCTCCGCCACCTCTACCAGGGCTGCCAGGTGGTGCAGGGAAACCTG	180
Qy	61 GluLeuThr	TyrLeuProThrAsn.	AlaSerLeuSerPheL	euGlnAspileGlnGluVal	80
Db 1	81 GAACTCACC	TACCTGCCCACCAAT	GCCAGCCTGTCCTTCC	GAACTCACCTACCTGCCCACCAATGCCAGCCTGTTCCTTCC	240
Qy	81 GlnGlyTyr	ValLeuIleAlaHis	AsnGlnValArgGlnV	alProteuGlnArgLeuArg	100
Db 2	41 CAGGGCTAC	GTGCTCATCGCTCAC	AACCAAGTGAGGCAGG	CAGGGCTACGTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGTGCAGGCTGCGG	300
0y 1	01 IlevalArg	GlyThrGlnLeuPhe	GluAspAsnTyrAlaI	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Dp	01 ATTGTGCGA	GGCACCCAGCTCTT	GAGGACAACTATGCC	TGGCCGTGCTAGACAATGGA	360
Qy 1	21 AspProLeu	ASDASDThrThrPro	ValThrGlyAlaSerF	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db 3	61 GACCCGCTG	AACAATACCACCCCT	GTCACAGGGGCCTCCC	CAGGAGCCTGCGGGAGCTG	420
Qy 1	41 GlnLeuArg	SerLeuThrGluile	LeuLysGlyGlyVall	eulleGlnArgAsnProGln	160
Db 4	21 CAGCTICGA	AGCCTCACAGAGATC	TTGAAAGGAGGGGTCT	CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	480
Qy 1	61 LeuCysTyr	LeuCysTyrGlnAspThrIleLeuTrpLysAspIl	TrpLysAspilePhen	9 -	180
Db 4	81 CTCTGCTAC	CAGGACACGATTTTG	TGGAAGGACATCTTCC	CTTCCACAAGAACAACCAGCTGGCT	540
0y 1	81 LeuThrLeu	(IleaspThrasnarg	SerArgAlaCysHisF	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Dp 2	41 CTCACACTG	ATAGACACCAACCGC	TCTCGGGCCTGCCACC	CCTGTTCTCCGATGTGTAAG	009
Qy 2	201 GlySerArg	CysTrpGlyGluSer	SerGluAspCysGlnS	SerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
pp qq	01 GGCTCCCGC	TGCTGGGGAGAGT	TCTGAGGATTGTCAGA	GCCTGACGCGCACTGTCTGT	099
0y 2	21 AlaGlyGly	CysAlaArgCysLys	GlyProLeuProThrA	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
9 qa	61 GCCGGTGGC	TGTGCCCGCTGCAAG	GGGCCACTGCCCACTG	ACTGCTGCCATGAGCAGTGT	720

1020 1080 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 400 420 440 460 480 500 520 540 260 580 260 780 280 840 300 900 320 960 340 360 380 009 GAGGTGACAGCAGAGGATGGAACACAGGGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1021 GTGTGCTATGGTCTGGGGCATGGAGCACTTGCGAGAGGTGAGGCAGTTACCAGTGCCAAT AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValḤisThrVal 196 1081 381 441 481 1441 501 521 1561 1621 241 721 461 501 1681 781 841 901 341 541 561 281 301 581 261 321 g g g g ò g ŏ Q δy g δy DB ö qq ò Dp à d d ò Qγ d g à g ò Ω g δ g g ô ò δ à ò

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SEQ7 (1-	712)	x AAA09455	(1-3768)			
oy.	1	MetGluLeuAlaAlaLe	uCysArg	TrpGlyLeuLeuLeuAlaLe	AlaLeuLeuProProGlyAla	
අු		ATGGAGCTG	GTGCCGC	999	CTIGCCCCCCGGAGC	09
δλ	_	AlaSerThrGlnValCy	GlnValCysThrGlyThrAs	ThraspMetLysLeuArg	ArgLeuProAlaSerProGlu	40
Dβ	61	GCGAGCACC	CAAGTGTGCACCGGC	ACAGACATGAAGCTG	CTCCCTGCCAGTCCCGA	120
Qy Dp	41	ThrHisLeu ACCCACCIG	ThrHisbeuAspMetLeuArgHis 	rgHisLeuTyrGlnGlyCysGlnVal 	SInvalvalGinglyAsnLeu 	60
Qy	61	GluLeuThr	TyrLeuProThrAsn	AlaSerLeuSerPhe	eGlnGluVa	0
qa	181	GAACTCACC	GAACTCACCTACCTGCCCACCAATGCCA	GCCAGCCTGTCCTGCAGGATAT	CTGCAGGATATCCAGGAGGTG	240
Οy	81	GlnGlyTyr	ValLeuIleAlaHis	GlyTyrValLeuIleAlaHisAsnGlnValArgGlnVa	1ProLeuGlnArgLeuAr	100
Db	241	CAGGGCTAC	GTGCTCATCGCTCAC	AACCAAGTGAGGCAG	STCCCACTGCAGAGGCTGCGG	300
Qy	101	IleValArg	GlyThrGlnLeuPhe	leValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLe	uAlaValLeuAspAsr	120
Dp	301	ATTGTGCGA	GGCACCCAGCTCTTT	GAGGACAACTATGCC	CTGGCCGTGCTAGACAATGGA	360
0y	7	AspProLeu 	AsnAsnThrThrPro	OLEUASnAsnThrThrProValThrGlyAlaSerProGly 	ProGlyGlyLeuArgGluLeu	4
QQ			AACAATACCACCCCT	GTCACAGGGGCCTCC	CCAGGAGGCCTGCGGGAGCTG	42
Qy	141	GlnLeuArg	SerLeuThrGluIle	euArgSerLeuThrGluIleLeuLysGlyGlyValLeuIl\	LeuIleGlnArgAsnProGln	16
ΟĎ	421	TCGA	AGCCTCACAGAGATC	TTGAAAGGAGGGGTC	TTGATCCAGCGGAACCCCCAG	480
oy G	161	LeuCysTyr(3lnAspThrIleLeu	TrpLysAspIlePhel	GlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	ω -
e :		CTAC	CAGGACACGATTTTG	regaaggacarcite	CACAAGAACAACCAGCTGGCT	4 (
දු දු	541	Leurnreeu 	lleaspinrasnarg 	SerArgAlaCysHisl 	IIII	200
Qy	201	GlySerArg(CysTrpGlyGluSer	SerGluAspCysGln	SerLeuThrArqThrValCys	Ñ
qq	601	GGCTCCCGC				9
QY	221	laGly	CysAlaArgCysLys	SlyProLeuProThri	ysHisGluGlnCy	240
qα	661	GCCGGTGGC	GGCTGTGCCCGCTGCAAGGGGCCCACTGCC	GGGCCACTGCCCACTC	CACTGACTGCTGCCATGAGCAGTGT	720
Qy	241	AlaAlaGlyCys	CysThrGlyProLysHisSe	rAspCys	SLeuAlaCysLeuHisPheAsnHis	260
qa	721	GCTGCCGGC	ACGGG	TGACTG	CTCCACTTCAACCA	780
. 60	261	SerGlyIleCysG	CysGluLeuHisCys	GluLeuHisCysProAlaLeuValThrTyrAsnThrAspThr	<pre>PyrAsnThrAspThrPheGlu </pre>	280
Dþ	781	AGTGGCATC	rereaecrecacrec	casccrastracc	rTTGA	840
Qy	α	erMetPr	oAsnProGluGlyArgT	yrThrPheGlyAla	SerCysValThrAlaCysPro	300
qa		· Ö	sassecces	ATACATICGGCGCC	AGCTGTGTGACTGCCTGTCC	006
Qy	301	TyrAsnTyrl	rLeuSerThrAspVal(GlySerCysThrLeuV	/alCysProLeuHisAsnGln	320

1140 1200 1440 1500 1560 1620 1080 1260 1320 1380 1680 1740 1860 1920 1980 520 540 1800 340 360 380 400 420 440 460 480 500 560 580 620 640 960 900 653 653 GluvalthralaGluaspGlythrGlnargCysGluLysCysSerLysProCysAlaArg ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro GlyCysProAlaGluGlnArgAlaSerProLeuThrSer---1021 1141 1201 1261 1321 1441 1501 1561 1621 1681 1741 1801 1861 1921 901 321 961 341 381 401 421 441 481 501 521 541 561 581 601 621 641 653 ò g QY g Οy q οy Db οy Op δ g ò g ò O οy q $^{\circ}$ Ob δy a δy Q δý g ò g ÓΥ P δ g οy g ò

Qy	653 653	
QQ	2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2100	3121
δ	653 653	SULT 5 H23392
QQ	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGGTGCGGATCCTGAAAGAGACGGAGCTG 2160	
0y	653 653	AAH23392;
QQ	2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	25-SEP-2001 (fi
ογ	653 653	Human HER-2/neu pi
qq	2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280	KW Antigen-presenting cell; KW oncogene; cancer; cytost
ογ	653 653	OS Homo sapiens.
q	2281 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2340	Key
ογ	653 653	SCDS
g	2341 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACCTT 2400	
οý	653 653	
qq	2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460	26-JUL-2001.
ογ	653 653	19-JAN-2001;
οp	2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520	21-JAN-2000; 20
Οy	653 653	(CORI-) CORI
qa	2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580	
ογ	653 653	DR WPI; 2001-476112/51. DR P-PSDB; AAB85458.
අු	2581 ATTACAGACTTCGGGCTGGCTGGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640	New antigen-
ογ	653 653	PT for treating or preventing
QΩ	2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2700	AA
ογ	653 653	
QQ	2701 CACCAGAGTGATGTGTGGGGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2760	CC expresses at least an imm
οy	653 653	
q	2761 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG 2820	
٥'n	653 653	CC encoding the human HER-2,
qq	2821 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 2880	XX SQ Sequence 3768 BP; 759 A;
٥y	653 653	Alignment Scores:
qq	2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 2940	
0y	654	Best Local Similarity: 67.948
qq	2941 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCCAGTCCTTG 3000	
οy	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspWetGlyAspLeuValAspAla 684	SEQ7 (1-712) x AAH23392 (1-376
qq	3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT 3060	Qy 1 MetGluLeuAlaAlaI
δ	685 GluGluTyrLeuvalProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704	Db 1 ATGGAGCTGGCGGCC
QQ O	3061 GAGGAGTATCTGGTACCCCAGCAGGGTTCTTCTGTCCAGACCCTGCCCGGGCGCTGGG 3120	Qy 21 AlaSerThrGlnVald

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an isolated antigen-presenting cell, which lumunogenic portion of a polypeptide that produces STRE 2/neu protein. The antigen-presenting cells are eliciting or enhancing an immune response to itcularly in treating or preventing malignancies in preventing cancer, e.g. breast cancer, ovarian, preventing cancer, e.g. breast cancer, ovarian, a cancers. The present sequence represents a DNA -2/neu protein (also known as p185 or c-erbb2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells, useful as vaccines for eliciting or
ponse to HER-2/neu protein, particularly useful
ing cancer, e.g. breast cancer
                                                                                                                                                                                                                                                                     ; immunogenic; immune response; HER-2/neu; tatic; vaccine; p185; c-erbB2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 1171 C; 1119 G; 719 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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t= "HER-2/neu protein"
isarghisarg 712
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acaggcaccgc 3144
                                                                                                                                                                                                                                 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                   n/Qualifiers
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                    2281 CCCAAAGCCAACAAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA
                                                2341 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACATT
                                                                            2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG
                                                                                                        2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG
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The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRMAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand(sl, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by Plasmodlum or viruses/viroids (pathogenic on humans, animals or plants). The method incovides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is with interferon. The present sequence is that of a target DNA of the
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                                                                                                                                                                                                                                                                                                                                                            by introducing into cells two double-stranded RNAs that are complementary to the target
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human; HIV; human immunodeficiency virus; papilloma virus; gene; ds.
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Matches:
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                      virus; human
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                                                                                                                                                                                                                                                                (RIBO-) RIBOPHARMA
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SASNGIY 12 AATGGA 36	uArgGluLeu 140 	gAsnProGln 160 	GlnLeuAla 180 	омеtCysLys 200 GATGTGTAAG 600	ThrValCys 220 ACTGTCTGT 660	GluGlnCys 240 GAGCAGTGT 720	isPheAsnHis 260 actrcaaccac 780	pThrPheGlu 280 	AlaCyspro 300 	HisAsnGln 320 cacaaccaa 960	oCysalaarg 340 	Seralaasn 360 AGTGCCAAT 1080	euProGluser 380 	uGlnValPhe 400 CCAAGIGITI 1200	ipSerLeuPro 420 CAGCCIGCCT 1260	SASNGlyAla 440 CAATGCCCC 1320	erLeuArgGlu 460
ASDTYTALALEUALAVALLE	31yAlaSerProGlyGlyLe 	31yG1yValLeuIleGlnAx 	SASDIlePheHisLysAsnAsr 	aCyshisProCysSerPr : :crGcCACCCTGTTCTCC	SerGluaspCysGlnSerLeuThrarg' TCTGAGGATTGTCAGAGCCTGACGCGC	oleuProThrAspCysCysHisG 	erAspCysLeuAlaCysLeuHis 	rAsnThras CAACACAGA	rPheGlyAlaSerCysValThrAla 	SThrLeuValCysProLeu 	1LysCysSerLysPr 	largGluvalargAlavalThrSerA 	ystystystlepheglySerLeualaPheLeu 	LeuGlnProGluGlnLe 	SerAlaTrpProAs 	ArgGlyArgIleLeuHi 	eSerTrpLeuGlyLeuArgSer
ArgGlyThrGlnLeuPheGluA 	beuAsnAsnThrThrProValThrC 	ArgSerLeuThrGluIleLeuLySC 	LeuCysTyrGlnAspThr11eLeuTrpLys 	LeulleAspThrAsnArgSerArgAl 	CystrpGlyGluSer 	GlyCysAlaArgCysLysGlyProLei 	31yCysThrGlyProLysHisS GCTGCACGGGCCCAAGCACT	IleCysGluLeuHisCysProAlaLeuValThrTy 	tProasnProgluglyargTyrThrPh 	TyrLeuSerThrAspValGlySerCy. 	GluValThrAlaGluAspGlyThrGlnArgCysGlu 	ystyrGlyLeuGlyMetGluHisLeuArgG 	3luPheAlaGlyC 	GlyAspProAlaSerAsnThrAlaPro 	LeuGluGluIleThrGlyTyrLeuTyrIle 	SerValPheGlnAsnLeuGlnValIle 	LeuThrLeuGlnGlyLeuGlyll
a — E	spProl	GlnLeu# 	Cys 	LeuThri CTCACAC	GlySerArg GGCTCCCGC	AlaglyC GCCGGTC	AlaAla(GCTGCC	erGly11e 	erMet []]]] CCATG	YrAsnTy 	uval GGTG	Valcys GTGTGC	Ilegln(ATCCAGG	Pheasp(TTTGATC	GluThr1 GAGACTC	AspleuSerV 	TyrSer

1981 ATTCTGCTGGTCGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2401 AFGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2281 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGCCTCCCCA 2341 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC

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target gene by introducing into the coll that contains the target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of trarget genes, particularly oncogenes, cytokine genes, Id (not define) protein genes; developmental or prion genes, or genes expressed in pathogenic corganisms (particularly plasmodia) or in viruses or virolds (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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                         Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon
                                                                                                                                                                                                                                                                                                                Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 other;
                                                                                                     This invention describes a novel method for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
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Matches:
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                                                                             Disclosure; Page 43-44; 98pp; German
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Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
qq	1741	AGTGTGTGTGTGTGTGTGTTTTTTGTGTGTGTGTGTGTG
Oy .	601	ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu 620
qq	1801	CTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGG
Qy	621	lyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuA
qq	1861	SATGCCAGCCTTGCCCCCATCAACTGCACCCCACTCTGTGTGTG
Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
Db	1921	CCCCCCGAGCAGAGCCAGCCTCT
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QQ	1981	ATTCTGCTGGTCGTGGTCTTGGGGGTGTTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040
Οy	653	653
Db	2041	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
Qy	653	653
Db	2101	ACACCTAGCGGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160
Qy	653	653
Db	2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
Qy	653	653
Db	2221	CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280
Qy	653	653
Db	2281	CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA 2340
Qy	653	
Db	2341	TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACGTT 2400
Qy	653	653
Db	2401	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460
Qy	653	653
QQ	2461	GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520
Qy	653	653
Db	2521	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
Qy	653	653
qq	2581	ATTACAGACTTCGGGCTGGCTGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
Qy	653	653
Db	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGG¢GGTTCACC 2700
Qy	653	653
Dp	2701	CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2760

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                                                                                                   CTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG
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/product- "Human HER2 protein"
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The invention relates to a transgenic non-human mammal that produces in its mammary gland cells detectable levels of a native human HER2 protein or its fragment. The transgenic animals are useful as tumour models for testing HER2-directed cancer therapies, and for identifying anticancer agents. The animals may also be used as source of cells which can be
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                                                                        immortalised in culture, in screening for compounds that have potential as prophylactic or therapeutic treatments of diseases or disorders involving expression of HER2. The anti-cancer molecules are useful for inducing appetosis or cell death of cancer cells. The present sequence is human HER-2 coNA.
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Matches:
Conservative:
Mismatches:
Indels:
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3776.00
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21 GCTGCCGG	CTGCACGGGCCCCAAGCACTCTGACTGCCTGGCCTGCCTCCACTTCAACCAC 780	
261 SerGlyI 781 AGTGGCA	IleCysGluLeufisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280 	
1 SerMet	CysPro 30 GTCCC 90	
301 Tyrasn 1 1 1 	yrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 	
21 Gluva] 61 GAGGTC	ThralagluaspGlyThrGlnargCysGluLysCysSerLysProCysAlaArg 340 	
341 ValCy: 021 GTGTG	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360 	
61 11egli 81 ATCCA	eGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380 	
381 PheAs 111	PheaspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400 	
401 GluTh 201 GAGAC	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420 	
421 ASPLE 261 GACCT	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440 	
441 TyrSe 321 TACTO	TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuargGlu 460 	
61 LeuGl 81 CTGGG	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCySPheValHisThrVal 480 	
81 Profit 	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500 	
501 GluA 501 GAGG	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520 	
521 TrpG 561 TGGG	rpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 	
541 ValG] 	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560 	
561 LeuP 681 TTGC	euProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 	
81 Alaas 41. GCTG2	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 	
01 Prose 01 CCCAG	roSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620 	·

	621 1861	GlyalacysGlnProCysProIleasnCysThrHisSerCysValAspLeuAspAspLys 640
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	0	TCTGCTGGTCGTCGTCGCGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG
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	2041	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGGTGGAGGTGGAGCCGCTG 2100
	653	653
	2101	ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGGGAGCTG 2160
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	2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
	653	653
	2221	CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280
	653	923
	2281	CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2340
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	2341	TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACACCTT 2400
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	2401	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460
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	2461	GACCTGCTGAACTGGTGTATGCCAAGGGGGATGAGCTACCTGGAGGATGTGCGG 2520
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	2521	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
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	2581	ATTACAGACTTCGGGCTGGCTGGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
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	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGGGGTTCACC 2700
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	2701	CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
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	2761	AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2820
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	2821	CTGCCCCAGCCCCCATCTGCATGATGTCTACATGATCATGGTCAAAATGTTGGATG 2880
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                                                                                                                                                                               Human; immune response; T-helper cell epitope; chitosan; CTL response;
vaccine; prostate cancer; breast cancer; Her2 antigen; cytostatlc;
immunostimulant; gene; ds.
                                                                               AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla
                                                                                                  GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
  ----GlnAsnGluAspLeuGlyProAlaSerProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inducing or enhancing an immune response against an antigen, partitualarly cytotoxic T-lymphocyte responses, for treating or ameliorating prostate or breast cancer, comprises administering the antigen formulated with chitosan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/product= "Mature human Her2 antigen"
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03-NOV-2000; 2000US-245166P,
18-JUN-2001; 2001DK-0000936.
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                                                                                                                                                                                                                                                                           polypeptide antigen or its variant are useful in the preparation of an immunogenic composition for inducing or enhancing an immune response, particularly CTL response, against the polypeptide or protein antigen. The method for inducing or enhancing an immune response is useful in treating or ameliorating cancer, e.g. prostate or breast cancer. The
                                                                                                                                                                                          LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys
                                                                      T; 0 other;
                                                                                                    3768
712
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                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                      758 A; 1170 C; 1121 G; 719
                                                   present sequence is human Her2 antigen DNA.
                                                                                                   1.04e-235
3776.00
67.94%
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                                                                                                                                                                        (1-3768)
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Best Local Similarity:
                                                                      Sequence 3768
                                                                                          Alignment Scores:
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2941 AGGGACCCCCAGCGCTTTGT	r da	621 GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640
2881 ATTGACTCTGAATGTCGGCCAA	qa .	
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653	Qy	TIGCCGTGCCACCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 1
2761 AAACCTTACGATGGGATCCCAG	qq	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
653	Qy	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT 16
2701 CACCAGAGTGATGTGTGGAGTT	දි අ	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
2641 GGGGCCAAGGTGCCCATCAAGT	g .c	1561 IGGGGTCCAGGGCCCACCAGTGTGTCAACTGCAGCTTCCTTC
3	δy.	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
2581 ATTACAGACTTCGGGCTGGCTC	Op,	
653	Qy	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 5
2521 CTCGTACACAGGGACTTGGCCG	Db	
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2461 GACCTGCTGAACTGGTGTAT	qa	461 LeuclySerGiyLeuAlaLeulleHisHisAsnThrHisLeuCysPheValHisThrVal 480
653	Qy	INCITCACTION CONTROLL BOOK CALICACTION CALICACTICACTION CALICACTION CALICACTION CALICACTICACTICACTICACTICACTICACTICACTIC
2401 AIGCCCTAIGGCIGCCICII	Db	441 TyrSerLeufinfleufinGlyLeuflylleSerTrpLeuflyLeufrgSerLeuArgGlu 460
	Qy	GACCICAGCGICITCCAGAACCIGCAGIAAICCGGGGACGAATICIGCACAAIGGCGCC
2341 TATGTCTCCCGCCTTCTGGGCA	Db	440
653	Qy	SAGACTICTOGGAMGAGAT CACAGGTTACCTATACATCTCAGCCATGGCCTGGACAGCCTGCTT
2281 CCCAAAGCCAACAAAGAAATCT	QQ	401
653	δλ	
2221 CCTGATGGGGAGAATGTGAAAA	qq	THE
653	Qy	
2161 AGGAAGGTGAAGGTGCTTGGAT	QQ	
653	Qy	IleGlnGlupheAlaGlvCvstvsIvsIlepheGlvSertenAlapheTenDrogluSer 380
2101 ACACCTAGCGGAGCGATGCCCA	QQ	######################################
653	VO	20 - 1000000 100000000000000000000000000
2041 AAGATCCGGAAGTACACGATGC	qq	
653	Qy	
1981 ATTCTGCTGGTCGTGGTCTTGG	QQ	
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	7 1	snProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCys

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2940	1 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC	2881
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2880	1 CTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAÀTGTTGGATG	2821
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2820	1 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGGAGCGG	2761
653	3	653
2760	1 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC	2701
653	3	653
2700	1 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC	2641
653		653
2640	1 ATTACAGACTTCGGGCTGGCTCGCTGCTGGACATTGACGAGACAGA	258]
653	3	653
2580	1 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCAA	2521
653	3	923
2520	1 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG	2461
653	8	653
2460	ATGC	2401
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2400	1 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACGCTT	234
653	3	653
2340	1 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	228
653	3	92:
2280	1 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC	222
653	3	653
2220	1 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2161
653	3	653
2160	1 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACACGGAGCTG	2101
653	3	. 653
2100	1 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	204
653	3	65
2040	1 ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCAGCAG	198:
653	3	. 65.
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                                                                                                                                                                                                            RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to target and having an overhang -
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Conservative:
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                                                                                      3121 GGCATGGTCCACCACGCACGC 3144
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                                                                            GlyMetValHisHisArgHisArg 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene related to the invention.
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                                                                                                                                    ВР
                                                                                                                                                                                                                        virucide; protozoacide; gene;
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3776.00
67.94%
67.94%
95.50%
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                                                                                                                                                                                           ID NO 52
                                                                                                                                                                                                                                                                                                                   09-JAN-2001; 2001DE-1000586.
26-OCT-2001; 2001DE-1055280.
29-NOV-2001; 2001DE-1058411.
07-DEC-2001; 2001DE-1060151.
                                                                                                                                                                                                                                                                                                  2002WO-EP00152
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Limmer S,
                                                                                                                                                                                                                                                                                                                                                                    (RIBO-) RIBOPHARMA AG
                                                                                                                                                                                           Human ERBB2 DNA SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
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Best Local Similarity:
                                                                                                                                                                                                                                                            WO200255693-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3768
                                                                                                                                                                                                                                                                                                  09-JAN-2002;
                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                      Kreutzer R,
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                   3001
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DB:
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                                LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys
                                                                                                                                                                                                                                                                                                                                                     AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis
                                                                                                                                                                                                                                                                                                                                                                                                                        SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla
        101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
                                                                                                                                                                                                       AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu
                                                                                                                                                                                                                                                                                                                             CTCACACTGATAGACACCCACTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG
                                                                                                                                                                                                                                                                                                                                            GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys
                                                                                                                                                                                                                                                                                                                                                                             221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
                                                                                                    GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal
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The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human composition is useful for the therapy and diagnosis of cancer. The composition is useful for the therapy and diagnosis of cancer. The compositions for the diagnosis, prevention and transment of can do other compositions for the diagnosis, prevention and transment of thuman malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a patient. The invention is useful for stimulating a T cell response in a cumman patient, as probe or primer for nucleic acid hybridisation, to selectively form duplex molecules with complementary stretches of the entire Her-2/Neu gene or gene fragments of interest, to isolate a full complypatide in appropriate host cells. The composition is useful in prophylactic or therapeutic applications and for the treatment of cancer, preferably for the immunotherapy of breast cancer and other Her-2/Neu-composition is useful in gene therapy. The
                                                                                    Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated Her-2/Neu polypeptide composition useful for t
prevention and diagnosis of cancer, preferably breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foy IM, Lodes MJ,
                                                                                                                                                                                                                               Her-2/neu protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is human Her-2/neu protein DNA
                                                                                                                                                                                                                                                                               /noté= "Intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 109-114; 129pp; English.
                                                                                                                                                                        Location/Qualifiers
1.3768
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/product= "Human Her-
2026.3765
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hand-zimmermann S, Cheever MA,
Mcneill PD, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-225152P.
2000US-236428P.
2001US-270520P.
                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001WO-US41733
                                                   Her-2/neu protein DNA
                  (first entry)
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                                                                                                                                           Homo sapiens
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                  01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                    21-FEB-2002
                                                     Human
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(1-3768)

SEQ7 (1-712) x AAD32743

1021 GTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGGTGAGGGCAGTTACCAGTGCCAAT 1080 180 240 100 300 120 360 140 420 160 480 180 200 9 220 099 240 720 260 780 280 840 300 320 900 960 380 9 40 9 80 20 TyrAsnTyrLeuSerThrAspValG1ySerCysThrLeuValCysProLeuH1sAsnG1n LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal CTCTGCTACCAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACAACCAGCTGGCT GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 901 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCCCCTGCACAACCAA 841 961 41 121 61 181 101 301 121 361 421 481 181 541 201 601 221 661 241 721 261 781 301 341 141 161 281 321 g ò g ò g ò a δ q ò g οy g δ 6 Q Dp ò q Q D ò q οy g à g òγ g δy qq ò g ò g ò

XX DT 17-JUN-2002 (first entry)		•
92250;	Db 2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGGGGGAGCTG 2160	_ (
RESULT 12 ABA92250 ID ABA92250 standard: cDNA: 3	653 653	•
3121	Db 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGGTGGAGCCGCTG 2100	1
7	Ογ 653 653	•
3061	Db 1981 ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040	1
	Qy 653 653	5
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	Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653	J
2941	1861 GGGGATGCCAGCCTTGCCCATCAACTGCACCCACTCGTGTGGACTGACAAG	ц
Qy 654	621 GlyalaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 6	J
Db 2881 ATTGACTCTGAATGTCG	1801 CCCAGGGGGGGAAACCTGACCTACCTACATGCCCATCTGGAAGTTTCCAGAGGGG	. ப
Оу 653	6(1) Proger(1) vVallveDroßenlenGermynakeDrollomintvrDhobenhenlen(1), for	_
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Db 2761 AAACCTTACGATGGGAT	Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 bb 1681 mrccorncorn control of the cont	J
270	1621 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCAGG	
оу 653	541 ValGluGluCvsArqValLeuGlpGlvLeuProArgGluTvrValAsnAlaArgHisCvs 5	J
Db 2641 GGGGCAAGGTGCCCAI	VY 521 TIPOLIYPTOCLYFTOTINGATCYSSETGINPALCHARGGIVGINGLACYS 540	, 1
ОУ 653	101 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	- (
Db 2581 ATTACAGACTTCGGGCT	520	<i>-</i> ۱
Оу 653	1441 CCCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500	-
Db 2521 CTCGTACACAGGGACTT	481 ProTrpAspGlnLeuDheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	٠
DD 2461 GACCTGCTGAACTGGTG	Db 1381 CTGGGCAGTGGACTGGCCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTG 1440	1
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7	1321 TACTCGCTGACCCTGCAGGGCTGGGCATCAGCTGGCTGGGCTGCGCTCACTGAGGAA 1	ı
Оу 653	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArqSerLeuArgGlu 4	J
Db 2341 TATGTCTCCGCCTTC1	1261 GACCTCACCGTCTTCCACACCTGCAAATCCGGGGACGAATTCTGAATGCGCC	
Оу 653	A 21 And to Contral Dhod to the four four four four four four four four	
Db 2281 CCCAAAGCCAACAAGA	1201 GACACTCTCGAAGAGATCACAGGTTACCTATACTCAGGATGGCCGACAGCCTGCCT	
Оу 653	411 Clumbet outline littlembetel tomest outlines and consider the construction of the	
Db 2221 CCTGATGGGGAGAATG	SOL FRENSPELYASPELOMASSELASHIILALARTVOLENGIILETTILLILLILLILLILLILLILLILLILLILLILLILLIL	
Оу 653	1001 AICCROSAGIIIGCIGGCIGCAAAAAAAICIIIGGGAGCCIGGCAIIITCIGGGAGGGGGGGGGG	- (
Db 2161 AGGAAGGTGAAGGTGC	1,	_

2	1 1017	NGGAAGGIGAAGGIGCIIGGAGGCGCIIIIGGCACACAGICIACAAGGGCAICIGGAIC 2220
Qy	653	653
qq	2221 (CCTGATGGGGAGAATGTGGAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAAACACATCC 2280
Qy	653	653
qq	2281	CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCCA 2340
Oy	653	653
QC	2341 1	TATGICICCCCCTICTGGGCAICTGCCTGACATCCACGGTGCAGCTGGTGACACCTT 2400
Qy	653 -	653
Op	2401 ₽	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460
Oy	653 -	653
Ор	2461 6	GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520
·Oy	653 -	653
Dp	2521 0	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
Qy	653 -	653
QQ	2581 ₽	ATTACAGACTTCGGGCTGGCTGGCTGGCTGGACATTGACGAGACAGAGTACGATGCAGAT 2640
Qy	653	653
qq	2641 6	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGGGGTTCACC 2700
Qy	653 -	653
Dp	2701	CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGCC 2760
δλ	653 -	653
QQ	2761 #	AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2820
٥y	653 -	653
QQ	2821 0	CTGCCCCAGCCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 2880
ΟŸ	653 -	653
qq	2881 #	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCGGCATGGCC 2940
Qy	654 -	GlnAsnGluAspLeuGlyProAla;SerProLeu 664
Db	2941 P	AGGGACCCCCAGCGCTITGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAGCCATTG 3000
Qy	665 4	AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
QQ	3001	SACAGCACCTICTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT 3060
δy	685 (GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProdlyAlaGly 704
Op	3061	CTTCTGTCCAGACCCTGCCCCGGGCGCT
Qy	705 6	GlymetValHisHisArgHisArg 712
qq	3121	SCCATGGTCCACCACGCACCGC 3144
REST ABAS	RESULT 12 ABA92250 TD ABA92250	standard: cDNA: 3768 BP.
XX	2250:	
XX	1	

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vaccine; tyrosine kinase; ss.
                                     Location/Qualifiers
1..3768
/*tag= a
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                       cancer; tumour;
e therapy; gene;
Oct 17 07:48:14 2003
                          gene therapy;
                       oncogene;
                  Her-2/neu cDNA
                                sapiens
                       Her-2/neu;
                          receptor;
                  Human
                                Homo
                                     Key
Fri
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2001WO-US24283 03-AUG-2000; 2000US-0632507 03-AUG-2001;

WO200212341-A2

14-FEB-2002

BIOLOGICALS SMITHKLINE BEECHAM (CORI-) CORIXA (SMIK) SMITHKI

Gheysen D; ₩ Y Cheever

WPI; 2002-241743/29 P-PSDB; AAM51143.

eliciting Her-2/neu fusion protein for treating or preventing cancer by or enhancing an immune response to the protein, has Her-2/neu extracellular domain fused to Her-2/neu intracellular or phosphorylation domain

Disclosure; Fig 15; 141pp; English.

The present sequence is that of human Her-2/neu oncogene CDNA.
The CDNA encodes Her-2/neu (p185), an oncogenic self protein and target for anti-cancer vaccines. The Her-2/neu gene is amplified and p185 is overexpressed in a variety of cancers, including breast, ovarian, colon, lung and prostate cancer. Her-2/neu is a member of the tyrosine kinase family of receptor-like glycoproteins.

Its overexpression correlates with a poor prognosis in breast and ovarian cancers. The invention provides Her-2/neu fusion proteins proteins proteins or nucleic acid molecules. In preferred fusion proteins or nucleic acid molecules. In preferred fusion proteins or nucleic acid molecules. In protein is fused to a Her-2/neu intracellular domain of a Her-2/neu protein is elicited or enhanced by campistering the fusion protein is elicited or enhanced by administering the fusion protein is elicited or enhanced by campistering the fusion protein and delivering the transfected cells concoding the fusion protein, and delivering the transfected cells concoding the fusion protein, and delivering the transfected cells concoding the fusion protein, and delivering the development of a cancer. Specific T-cells are useful for inhibiting the development of a cancer cancer especially breast, ovarian, colon, lung or prostate cancer in a patient. T cells that specifically react with a Her-2/neu fusion protein encoded the sample in development of cancer in a patient. order to inhibit the

BP; 759 A; 1171 C; 1119 G; 719 T; 0 other; Sequence 3768

3768 712 0 0 336 Length: Matches: Conservative: Mismatches: Indels: Gaps: 1.04e-235 3776.00 67.94% 67.94% 95.50% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: .. 0 Score:

MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20

(1-712) x ABA92250 (1-3768)

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140 540 220 120 180 240 100 300 120 360 420 160 480 180 200 900 99 260 780 280 840 300 900 320 960 340 380 40 9 80 9 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla AlaSerThrGlnValCysThrGlyThrAspMetLySLeuArgLeuProAlaSerProGlu 61 GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGCTCCCTGCCAGTCCCGAG ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGCTAGACAATGGA AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 21 41 181 241 101 301 121 161 721 781 301 901 961 61 81 361 141 481 181 541 201 601 661 241 261 281 841 321 341 1021 361 421 221 õ g q Qγ qq g ολ g Óγ qq ò g δy a δ qq ά QQ Ω g qq ò δ ŏ οy ò ŏ g δ qq δy g ò g à

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δÿ	381 PheaspGlyaspFroAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	S
q	1141 TITGATGGGGACCCAGCCTCCAACACTGCCCCCCTCCAGCCAG	an (
Οy	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420	ර් දි
qq	1201 GAGACTCTGGAAGAGTCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT	3 8
ογ	421 AspLeuSerValPheGlnAsnLeuGlnVallleArgGlyArgIleLeuHisAsnGlyAla 440	Š
qq	1261 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGGACGAATTCTGCACAATGGCGCC 1320	3 8
٥y	441 TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	3 E
qq	1321 TACTCGCTGACCCTGCAAGGGCTGGGCTCAGCTGGGCTGCGGCTCACTGAGGGAA 1380	3 8
ζ	461 LeuGlySerGlyLeuAlaLeuIleH18H18H3ASnThrH18LeuCySPheValH18ThrVal 480	; E
g G	1381 CIGGGCAGIGGACIGGCCCICAICCACATAACACCCACCICIGCIICGIGCACACGGIG 1440	2 6
٥y	481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	ÿ
Dp	1441 CCCTGGGACCACCTCTTCGGAACCGCACCAACCTCTGCTCCACACTGCCAACCGGCCA 1500	3 6
٥y	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 5	7 A
QQ	1501 GAGGACGAGTGTGGGGCGAGGGCCTGGCCACCAGCTGTGGGCCCCGAGGGCACTGC 1560	è
Οy	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540	ž 2
ф	1561 TGGGGTCCAGGCCCACCCAGTGTGTGAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620	3 :
δy	541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHiSCys 560	÷ 5
qq	1621 GTGGAGGAATGCCGAGTACTGCAGGGGTTCCCCCAGGGAGTATGTGAATGCCAGGCACTGT 1680	3 :
Qy	561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580	Š
qq	1681 TTGCCGTGCCACCCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG 1740	a :
Qy	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	δ
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Οy	621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640	Ž i
QQ	1861 GGCGCATGCCAGCCTTGCCCCATCAACTGCACCCCCTGTGTGGACCTGGATGACAAG 1920	gn .
δy	641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer653	δδ
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qq	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGGATCCTGAAAGAGAGGGGGGTG 2160	ID ABKI
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QQ	2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCAGTCTACAAGGGCATCTGGATC 2220	DT 05-0

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QQ	D 2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGT	rgagctacctggaggatgtgcgg 2520
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Qy	у 653	653
qq	b 2761 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGAC	ACCTGCTGGAAAAGGGGGGGGGG 2820
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Dp	b 2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTGTGAATTCTCCGGCATGGC	rgtctgaattctcccccatgcc 2940
QY	654	spleuglyProAlaSerProLeu 664
QQ	b 2941 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGC	ACTIGGCCCCAGCCAGTCCCTIG 3000
δ	y 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla	spMetGlyAspLeuvalAspAla 684
QQ	3001	ACATGGGGACCTGGTGGATGCT 3060
ΟŸ	y 685 GluGluTyrLeuValProGlnGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	roAspProAlaProGlyAlaGly 704
qq	3061	SAGACCCTGCCCGGGCGCTGGG 3120
Qy	y 705 GlyMetValHisHisArgHisArg 712	
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                                                                                                                                                                                                                                                                                                                                                    Inhibiting haematological malignancy development by administering polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide encoding the polypeptide, or antigen presenting cells expressing the
                      Human; Her-2/neu; gene; ds; cytostatic; haematological malignancy; CML; acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL; chronic lymphocytic leukaemia; myeloma; non-Hoddykin's lymphoma; MDS; Hoddykin's lymphoma; T cell therapy.
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1411 CTOTATORAGEACTOCACACACACACACACACACACACACACACACACACA	0y	LeuGlySerGlyLeuAlaLeuIleHisHisHsnThrHisLeuCysPheValHisThrVal	· da	2461 GACCTG
41 ProTryApaColLinguith Data 1992 Profits 111	ga	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACC	٥٥	
1411 CCCTGGGGCCACCACCACCACCACCACCACCACCACCACCACCA	δλ	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	7 A	2521 CTCGTA
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1501 AGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Οy	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	Z qq	2581 ATTACA
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1561 TGGGGTCCAGGGCCCACCAGTGTTCCATCGGGGCCAGGAGTGC 150	δλ	TrpGlyProGlyProThrGlnCysValasnCysSerGlnPheLeuArgGlyGlnGluCys	1 8	2641 GGGGGC
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641 GlyCysProAlaGluGInArgAlaSerProLeuThirSer	7 음		q a	2941 AGGGAC
1921	Qy	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	Qy	665 AspSer
653 09 1981 ATTCTGCTGGTCGTGGTGTTTGGGGTCTTTGGGATCCTCATCAAGCGACGCAG 2040 09 653 09 09 09 653 09 09 09 653 09 09 2041 AAGATCCGGAGGTGCTGCTGCAGAACCGAGCTGGTGGTGGTGCTGCTGGTGGTGGTGGTGGTGGTGGTG	Db		qa	
1981 ATTCTGCTGGTCGTGGTCTTTGGGATCCTCATCAAGCGACGC 2040 653	δy		Oy	685 GluGlu
653 097 2041 AAGATCCGGAAGTACCGAGCCGCAGGAACCGCAGCCGCCGCTG 2100 RESUL 653	Db	ATTCTGCTGGTCGTCGTCTTTGGGGTCGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	q a	
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101 ACACCTAGCGGAGCGATGCCGAGCGGAGTCCTGAAAGAGAGGGGGCTG 2160 XX 653	QY		RESUI ABL91	
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653	Dp	CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC	X X	
2281 CCCAAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGGGCTCCCCA 2340 XX 653	δλ		XX	
653 653 XX 2341 TATGTCTCCCCCCTTCTGGCCACCTGACATCCACGGTGCAGCTGGTGACACACGTT 2400 XX	Db	CCCAAAGCCAACAAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	S X S	Homo sapiens.
2341 TATGICTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGGTGGTGACACACGTT 2400 XX	Qy			DELUIOUS88-CI.
	qa	TATGTCTCCCGCCTTCTGGCCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT	- XX	11-APR-2002.

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Db	2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACGGCGGACGCCTGGGCTCC	ACCGCGGACGCCTGGGCTCCCAG 2460
Qy		
qq	2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG	rgagctacctggaggatgtgcgg 2520
QY		
QQ	2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGGTGAAGAGTCCCAACCÀTGTCAAA	CCAAGAGTCCCAACCATGTCAAA 2580
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qq	2581 ATTACAGACTTCGGGCTGGCTCGGCTGCACATTGACGAGACAGAGTACCAT	ACGAGACAGAGIACCAIGCAGAI 2640
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qq	2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC	CATICICCGCCGGCGGTTCACC 2700
Qy		653
qq	2701 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGGAGCTGATGACTTTTGGGGCC	SGGAGCTGATGACTTTTGGGGCC 2760
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qq	2761 AAACCTTACGATGGGATCCCAGCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG	ACCTGCTGGAAAAGGGGGAGCGG 2820
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QQ	2821 CTGCCCCAGCCCCCATCTGCACCATGATGTCTACATGATCATGGTCAAATGTTGGATG	RGATCATGGTCAAATGTTGGATG 2880
Qy	, 653	
qq	2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTCTGAATTCTCCCGGCATGGCC	GICIGAATICICCGGCAIGGCC 2940
οy	654	spreuGlyProAlaSerProLeu 664
qq	2941	ACTIGGCCCAGCCAGICCCITG 3000
Qy	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAl	spMetGlyAspLeuValAspAla 684
qq	3001	ACATGGGGGACCTGGTGGATGCT 3060
ογ	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspFroAlaFroGlyAlaGly	coAspProAlaProGlyAlaGly 704
qq	3061	AGACCCTGCCCGGGCGCTGGG 3120
Qy	705 GlyMetValHisHisArgHisArg 712	
qa	3121	
RESU ABL9 ID	RESULT 14 ABL91709 ID ABL91709 standard; DNA; 3768 BP.	
AC :	ABL91709;	
X LO	28-MAY-2002 (first entry)	
S E S	Human polynucleotide SEQ ID NO 52.	
X X X	Human; HIV; HCV; gene expression; oligoribonucleotide Plasmodium; virus; viroid; cytokine; prion; antisense Cytostatic; virucide; protozoacide; antibacterial; ds	eotide; tumour; pathogen; isense oligonucleotide; al; ds.
XX OS	Homo sapiens.	
X A	DE10100586-C1.	

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CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG
                    LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla
                               SerGlyIleCysGluLeuH1sCysProAlaLeuValThrTyrAsnThrAspThrPheGlu
                                                                                                                                                                                                                                 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro
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                                                                                                                                                       The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oilgoriboniclectide that has a double-stranded structure consisting of a most 49 sequential nuclectide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oilgoribonuclectides for antisense inhibition of gene expression useful e.g. for treating tumours but the oilgoribonuclectides may also be viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oilgonuclectides, probably because the unpaired overhang increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for e.g. treating tumors, oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly
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Mismatches:
Indels:
Gaps:
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complementary
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Matches:
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                  09-JAN-2001; 2001DE-1000586
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Best Local Similarity:
Query Match:
DB:
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introducing d
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Score:
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PA (ERIC/) ERICKSON S. PA (SCHW/) SCHWAII. P	2581 ATTACAGACTTCGGGCTGGTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640	Dp
PR 16-MAR-2000; 2000US-189844P. PR 05-OCT-2000; 2000US-238327P. xx	653 653	Qy
16-MAR-2001;	2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580	QQ
	653 653	Qy
	2461 GACCTGCTGAACTGGTGTATGCAAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520	qq
	653	Qy
CDS 13768 /*tag= a	2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGGTCCCAG 2460	qa
XX XX FH Key Location/Quali	653 653	QY
OS Homo sapiens.	2341 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2400	QQ
	653 653	Qy
	2281 CCCAAAGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGGCTCCCCCA 2340	qa
KW thyroid; pancheas; prostate; b	653 653	δλ
KW Human; HEKZ; ErbB; epidermal g: KW anti-ErbB antibody-maytansinoi	2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280	QQ
Human HERZ (ErDBZ)	653 653	δδ
23-APR-2002 (IIISU	2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220	qa
ABK14038;	653 653	Qy
	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGGGAGCTG 2160	qq
K14058	653 653	QY
1710	2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100	qa
Qy /OS GIYMETVALHISHISATGHIS	653 653	QY
3002	1981 ATTCTGCTGGTCGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCAGCAG 2040	qa
	653 653	Qy
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DD 2941 AGGACCCCCAGCGCTTTGTG	621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640 [oy a
654	1801 CCCAGCGGTGTGAAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860	qa
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Db 2761 AAACCTTACGATGGGATCCCA	JOI DEUKTOOVSHISKIOOLUOVSBOINKIOOLINKSHOLYSERVALTIIROVSKREGIYYLOOTU SBU 	දි සි
Оу 653	GIGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT	a d
7	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	δŏ
653	1561 TGGGGTCCAGGGCCCACCCAGTGTGTCAACTGCAGCCAGTTCGTTC	QQ
OY 653	521 TrpGlyProGlyProThrGlnCysValAsnCySSerGlnPheLeuArgGlyGlnGluCys 540	Qy

Qy	653 653
qa	2641 GGGGGGAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2700
QY	653 653
qq	2701 CACCAGAGTGATGTGTGTGATTATGGTGTGTGTGTGGGGAGCTGATGACTTTTTGGGGGCC 2760
QY	653 653
qa	2761 AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2820
QY	653 653
qa	2821 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 2880
QY	653 653
qa	2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTGTGAATTCTCCCGCATGGCC 2940
Οy	654
qq	2941 AGGGACCCCCAGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG
ΟY	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
qq	3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT 3060
δy	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
QQ	3061 GAGGAGTATCTGGTACCCCAGCAGGGCTTCTTCTGTCCAGACCCTGCCCCGGGCGCTGG 3120
Qy	705 GlyMetValHisHisArgHisArg 712
qq	3121 GGCATGGTCCACACAGGCACGC 3144
RESULT ABK1405	RESULT 15 ABK14058 TD ARK14058 standard: CDNA: 3768 RD
XX	
X	
TO X	23-APR-2002 (first entry)
DE	Human HER2 (ErbB2) cDNA.
X	
KW	<pre>antl-Erbb antibody-maytansinoid conjugate; cancer; tumour; breast; ovary; stomach; endometrium; salivary gland; lung; kidney; colon; colorectum;</pre>
K K	thyroid; pancreas; prostate; bladder; ErbB2; neuronal disorder;
X X X	ging usouver; astrocytal disolder; hypothalamic disolder; glandular disorder; macrophagal disolder; epithelial disorder; ctromal disorder; blattocolia disorder; disorder;
KW	angiogenic disorder; immunological disorder.
4 8 8	Homo sapiens.
FH I	Key Location/Qualifiers
F F	CDS 13768 /*tag= a
FT	/product= "Human HER2"
Nd	US2002001587-A1.
X G	03-JAN-2002.
AA PF	16-MAR-2001; 2001US-0811123.
PR PR	16-WAR-2000; 2000US-189844P. 05-OCT-2000; 2000US-238327P.
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                                                                                                                               is characterised by the overexpression of an epidermal growth factor with an anti-ErbB antibody comprising administering to treatment with an anti-ErbB antibody comprising administering to treatment anti-ErbB antibody maytensing administering to method is useful for treating cancer or tumours of the breast, ovary, stomach, endomerrium, salivary gland, lung, kidney, colon, colorectum, thyroid, pancreas, prostate and bladder, preferably breast cancer. The breast cancer is a metastatic breast cancer or an aggressive form of metastatic breast cancer which overexpresses ErbB2. The method is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and
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                                                               Treating tumour characterised by overexpression of epidermal growth factor receptor, ErbB or cancer in mammal, comprises administering
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anti-ErbB antibody-maytansinoid con
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Patent: WO 0153463-A 1 26-JUL-2001;
CORIXA CORPORATION (US)
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DLGWGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVR
PQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGGAA
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Matches:
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Best Local Similarity:
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CDS

Qp	181 LeuThrLeulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200 181 -	7 A	1621 GTGGAGGAATGCCGAGTACTG
ογ	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	oy Op	561 LeuproCysHisProGluC:
DP QY	GCTGG	Qy	< − 0
QQ	661 GCCGGTGCTGTTGCTGCTGCAAGGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT 720	g å	
Ολ Dp	241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260 		1801 CCCAGGGGGGGAAACCTGAC
0У	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 28	Qy	621 GlyAlaCysGlnProCysProJ
qq	AGTGGCATCTGTGAGCTGCACTGCCCTGGTCACCTACAACACACAC	0y	641
Qy Db	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300 	qq	
δλ	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 3	δλ	653
dū .	901 TACAACTACCTTTCTACGGACGTGGGATCCTGCACCCTCGTCTGCCCCCTGCACACAA 960	a , 8	1981 ATTCTGCTGGTCGTGGTCTT
δλ	GluvalThralaĠluaspGlyThrGlnargCysGluLysCysSerLysProCysAlaarg 340	QQ O	2041 AAGATCCGGAAGTACACGAT
Q	GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1	QY	- 1
g g	341 ValCysTyrClyLewGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360 	qa	2101 ACACCTAGCGGAGCGATGCC
)		QY	653
7 A		QQ	2161 AGGAAGGTGAAGGTGCTT
Οy	spproalaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	Oy	653
qq		qq	2221 CCTGATGGGGAGAATGTGAAAA
'n	luglulleThrGlvTvrLeuTvrlleSerAlaTrpProAspSerLeuDro 42	QY	653
qq		qO	2281 CCCAAAGCCAACAAAGAAAT
٥٨	alpheGlnAsnLenGlnVallleArgGlvArgIleLenHisAsnGlvAla 440	QY	653
r qq		qq	41
Ωÿ	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460	Oy	
qq		qa	01
Qy	461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480	Qy	653
QQ	4	qa	61
0y	481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	Qy	653
QQ		qq	21
٥y	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	δδ	653
qq		qq	81
٥y	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540	Qy	653
ź		qq	2641 GGGGCCAAGGTGCCCATCAAG

2y 3b	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
λ	561	euprocysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGl
ą	1681	CCCCAGAATGGCTCAGTGACCTGTTTTGGACCGG
λλ	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
ą	1741	CTGACCAGTGTGGCCTGTGCCCACTATAAGGACCCTCCCT
λ	601	ProSerGlyValLysProAspLeuSerTyrWetProlleTrpLysPheProAspGluGlu 620
ą	1801	CIGGAAGTITCCAGATGAGGA
λλ	621	GlyalaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
q	1861	GGC ATGC CAGC CTTGC CCCAT CAACTGC ACCCCACTC CTGTGTGACCTGGATGA
λλ	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer
q	1921	crecceeceagagagecagecerergaegree
λλ	653	653
q	1981	ATTCTGCTGGTCGTGGTCTTTGGGGTCTTTGGGATCCTCATCAAGCGACGCCAGCAG 2040
ίγ	653	653
ą	2041	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
λλ	653	653
q	2101	ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGAGGGGAGCTG 2160
λį	653	653
q	2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
λi	653	653
q	2221	CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280
γ	653	653
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λi	653	653
q	2341	TATGTCTCCCCCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGAČACAGCTT 2400
λi	653	653
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γ	653	653
q	2461	GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520
λi	653	653
qı	2521	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
, Āi	653	653
q	2581	ATTACAGACTTCGGGCTGGCTGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
λ	653	653
ą	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGGCGGCGGTTCACC 2700

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CQPQNGSYTCGPEALQCVACAHYRDPFCVARCPSGWRPDLSYMPTWRFDBEGGACQ
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PDGENVKIPVAIKVLRENTSPKANKEILDEAYWAGVGSPYVSRLLGICLTSTVQLVT
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                          CACCAGAGTGATGTGGGGGTTAATGGTGTGACTGTGGGGAGCTGATGACTTTTGGGGGCC
                                                                                                                 2821 CTGCCCCAGCCCCCCATCTGCATGATGTCTACATGATCATGGTCAAATGTTGGATG
                                                                                                                                                                                                                                                                         2881 ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC
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Her-2/neu fusion proteins
Patent: Wo 0212341-A 9 14-FEB-2002;
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS
Location/Qualifiers
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Sequence 9 from Patent WO0212341.
AX380923
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates;
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FCPDPARGAGGWYHHRRSSSTRSGGGDLTLGLEPSEERAPRSPLAPSEGAGSDYDG
DLGWGAAKGLQSLPTHDPSPLQNYSDPTVPLPSETDGYVAPLTCSPQPEYVNOPDVR
PQPPSPRBGPLPAARTALERPKTLSPGKNGVVKDVFARGGAVENPEYLFPQGGAA
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Mismatches:
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500	Ŝ	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600	Qy
2761 AAACCTTACGATGGGATCCCAGCCC	qa ::		qa
653	Oy	roGluCvsGlnProGlnAsnGlvSerValThrCvsPheGlvProGlu	ô
2701 CACCAGAGTGATGTGTGGAGTTAT	qa	######################################	S 8
653	Qy	TOGGGILCAGGGCCCAGIGIGICAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC	8 6
2641 GGGGGCAAGGTGCCCATCAAGTGGA	qa	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 11	ζ, dg
653	o 6	GAGGACGAGTGTGTGGGCGAGGCCTGCCTGCCACCAGCTGCGCCCCGAGGGCACTG	Dp
	О	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	0у
2521 CTCGTACACAGGGACTTGGCCGCTC	qa "		qq
653	Оў	481 ProrrpaspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500	Qy
61	qq		qq
653	δy	LeuGlySerGlyLeuAlaLeuTleHisHisAsnThrHisLeuCvsPheValHisThrVal 480	ò
2401 ATGCCCTATGGCTGCCTCTTAGACC	qa	44. ITAFSELENTALENGSINGLYLENGLYLLESETITPLENGLYLENALGSELENALGGGLU 460 	දු අ
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2341 TATGTCTCCGGCCTTCTGGGCATCT	QQ	421 AspleuserValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440 	yo da
653	Qy	GABAUTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCCT	ga
2281 CCCAAAGCCAACAAAGAAATCTTAG	qq	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	oy 4
	3 8	1141 TTTGATGGGGACCCAGCCTCCAACACTGCCCCGCTCCAGCCAG	qq
	S 1	381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400	QY
u u	a :	1081 ATCCAGGAGTTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGC 1140	qq
	λo	361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380	οy
2101 ACACCTAGCGGAGCGATGCCCAACC	qq		qq
653	QY	ValCvsTvrGlvLeuGlvWetGluHisLeuArcGluValArdalavalThrSeralaasn 360	ΛO
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653	Qy	1.C.C.161161CCC6661A1ACA11CGGCGCCACCAGCIG1G1GACIGCCIG1IGCC	3 8
1921 GCTGCCCGCCGAGAGACCC	qa —	281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300 [11	γο q
1861 GGCGCATGCCAGCCTTGCCCCATC	<u>a</u> :	781 AGTGGCATCTGTGCACTGCCCAGCCCTGGTCACCTACAACACACAC	qq
621 GlyAlaCysGlnProCysProIleA	δŏ	luLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPhe	Qy
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601 ProSerGlyValLySProAspLeuS	Qy	hrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 2	οy
	qa	661 GCCGGTGGCTGTGCCCCCTCCAAGGGCCACTGCCCACTGATGCTGCTGCCATGAGCAGTGT 720	qq
		221 AlaGlyGlyCysAlaArgCysLysClyProLeuProThrAspCysCysHisGluGlnCys 240	Qy

CCACTATAAGGACCCTCCCTTCTGCGTGGCCCGCTGC 1800 GGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040 AGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 2340 SAGACTGCTGCAGGAAACGGAGCTGGTGGÄGCCGCTG 2100 TGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220 TCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280 CCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460 TCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580 GCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640 GATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2700 TGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760 CCAGGCGCAGATGCGGATCCTGAAAGAGAGGGAGCTG 2160 CTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2400 SATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520 CCGGGAGATCCCTGACCTGCAAAAGGGGGGAGCGG 2820 653 653 653 653 653 653 653 653 653 ------ 653 aSerProLeuThrSer------

Alignment Scores: 1.32e-229 Length: 3768 Pred. No.: 3776.00 Matches: 712 Score: 67.94% Conservative: 0 Best Local Similarity: 67.94% Mismatches: 0 Query Match: 65.50% Indebs: 1 DB: 6	MetGluicualadlaleucysArgTrpGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuL
Db 2821 CTGCCCCAGCCCCCATCTGATGTCTACATGATCATGGTCAAATGTTGGATG 2880 Qy 653	Aspala 6 Garger 3 Alagly 7 Alagly 7

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1 ATTCTGCTGGTCGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2	653	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2	653	653 653 2281 CCCAAAGCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGTGGGCTCCCCA 2340	653 653 2341 TATGTCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGACACACAC	653 653 2401 ATGCCCTATGGCCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2460	653 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520	653 653 2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCCAACCATGTCAAA 2580	ATTACAGACTTCGGGCTGGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC	653 653 2701 CACCAGAGTGAGTGTGTGTGTGTGTGGGGGGCTGATGACTTTTGGGGCC 2760	AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCAGAAAAGGGGGGAGCGG	CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG	653	654	665 AspSerThrPheTyrargSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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	321 GluvalThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340 	341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360 	361 IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPh 	381 PheaspGlyAspProalaSerAsnThralaProLeuGlnProGluGlnLeuGlnValPhe 400	401 GluthrLeuGluGlullethrGlyfyrLeuTyrIleSerAlaTrpProAspSe 	421 AspLeuSerValPheGlnAsnLeuGlnVallleArgGlyArglleLeuHisAe 	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 	461 LeuGlySerGlyLeuAlaLeulleHisHisAsnThrHisLeuCysPheValHi 	481 ProTrpAspGlnLeuPheArgAs 	501 GluaspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGl 	521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540	31uCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlakr 	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600		621 GlyAlaCysGlnProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640 	41 GlycysprohlagluglnArgalaSerProLeuThrSer	
Q	Qy	Qy	Oy Db	Qy	Oy Dp	Oy Db	Qy	Qy Db	oy D	Qy	QY	Qy Db	Oy	QY	OY Db	Qy	Qy	QY

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GCGAGCACCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGGCTCCCTGCCAGTCCCGAG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Methods for diagnosis and therapy of l
virus-associated malignancies
Patent: WO 0213847-A 1 21-FEB-2002;
CORIXA CORPORATION (US)
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Sequence 1 from Patent W00213847.
AX465456
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                        GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg
                                                               CAGGGCTACGTGCTCATCGCTCACAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGCGG
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GluThrLeuGluGluI]eThrGlyTyrLeuTyrI]eSerAlaTrpProAspSerLeuPro	TACTCGCTGACCCTGCAAGGCTGGGCATCAGCTGGGGCTGGGGCTCCGCTCACTGAGGGAA LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal [[501 GluAsp6luCysVal6lyGlu6lyLeuAlaCysHisGlnLeuCysAlaArg6lyHisCys 520 1161111111111111111111111111111111111	561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580		1 ATTCTGCTGGTCGTCGTCGTGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2 3	2101 ACACCTAGGGGAGGGATGCCCAACCAGGGGATGCTGAAAGAGAGGGGTG 2160 653

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Matches:
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Db 1	1441 CCCTGGGACCAGGTCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500		į
QY	501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520	οy	
Db 1		Dp	2581 ATTA
2		QY	653
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2	541 valciuciucysargvalleucincifyleurroargelutfffvalasnalaarghiscys 560 	qa	2701 CACC
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Qy	621 GlyAlaCysGinProCysProlleAsnCysThrHisSerCysValAspLeuAspAspLys 640	ο _γ	
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δλ	653 653	RESULT 8 AX481438	
Db	2101 ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160	LOCUS	Z
Qy	653 653	ACCESSION VERSION	AX4814 AX4814
QQ	2161 AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGCCATCTGGATC 2220	KEYWORDS	
٥y	653 653	ORGANISM	Homo Eukar
qa	2221 CCTGATGGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2280	REFERENCE	
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δλ	653 653	Alignment S Pred. No.:	Scores:
QQ qq	2461 GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2520	Score: Percent S	Similarity
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Ob	2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580	: 20	

	Oy	653	653
	Db 2	581	ATTACAGACTTCGGGCTGGCTGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
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	Qy	653	653
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	Qy	653	653
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٥y	121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGly	3=	140	S 2
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٥y	161 LeuCysTyrGlnAspThrileLeuTrpLysAspil	ePheHisLysAsnAsnGlnLeuAla	180	ογ
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٥y	181 LeuThrLeulleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	SHisProCysSerProMetCysLys	200	ò á
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٥y	201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	'sGlnSerLeuThrArgThrValCys	220	Š á
qq	601 GGCTCCCGCTGCTGCTGCAGAGAGTTCTGAGGATTG	STCAGAGCCTGACGCGCACTGTCTGT	099	g :
٥y	221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	OThrAspCysCysHisGluGlnCys	240	à á
qq	661 GCGGTGGCTGTGCCCGCTGCAAGGGCCCACTGCC	CACTGACTGCCCATGAGCAGTGT	720	3 3
0y	241 AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	'sLeuAlaCysLeuHisPheAsnHis	260	Š 2
qa	721 GCTGCCGGCTGCACGGGCCCCAAGCACTCTGACTG	SCTGGCCTCCACTTCAACCAC	780	3 8
Οy	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	lThrTyrAsnThrAspThrPheGlu	280	Š É
QQ	781 AGTGGCATCTGTGAGCTGCACTGCCCAGCCCTGGT	CACCTACAACACAGACACGTTTGAG	840	3 8
Oy	281 SeIMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	.yAlaSerCysValThrAlaCysPro	300	Š ć
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oy.	301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	irLeuValCysProLeuHisAsnGln	320	ò i
qq	901 TACAACTACCTITCTACGGACGTGGGATCCTGCAC	CCTCGTCTGCCCCTGCACAACCAA	096	9 8
Οy	321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLy	uLysCysSerLysProCysAlaArg	340	5 6
qq	AGGT	GAAGTGCAGCAAGCCCTGTGCCCGA	1020	9 8
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qa	1021 GTGTGTATGGTCTGGGCATGGAGCACTTGCGAGA	GGTGAGGCCAGTTACCAGTGCCAAT	1080	3

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<u>۲</u>		heAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValP	400
ą	1141		1200
γ	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
ą	1201	BACTCTGGAAGAGTCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCCTGCC	1260
> 4	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 	1320
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a	1381	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACC	1440
γ	481	GlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnAr	200
Q	1441	CCTGGGACCAGCTCTTTCGGAACCCGCACCAAGCTCTGCTCCACCACCGGCC	1500
٨	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Q	1501	AGGACGAGTGTGTGTGGGCCGAGGGCCTGGCCTGCCACCAGCTGTGCGCCCCGAGGGCACTG	1560
*	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Ω	156i	GGGGTCCAGGGCCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCCAGGAGTG	1620
γ	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgH1SCys	260
Q	1621	TGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTG	1680
Y	9	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	280
Q	1681	tgccgtgccaccctgagtgtcagcccagaatggctcagtgacctgttttggaccgga	1740
γ	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	009
Д	1741	CTGACCAGTGTGTGGGCCTGTGCCCACTATAAGGACCCTCCTTCTGCGTGGCCCGCTG	1800
≻	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Д	1801	CCAGCGGTGTGAAACCTGACCTCCTACATGCCCATCTGGAAGTTTCCAGATGAGGA	1860
×	621	lyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAs	640
Q	1861	CGCATGCCAGCCTTGCCCCATCAACTGCACCCCACTCTGTGTGGACCTGGATGACAA	1920
λ	641	yCysProAlaGluGlnArgAlaSerProLeuThrS	653
, Q	1921	GCTGCCCGCCGAGCAGAGAGCCAGCCTCTGACGTCCATCGTCTC	1980
γ	653		653
Д	1981	ATTCTGCTGGTCGTCGTCGTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
λ	653		653
Ω	2041	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	2100
λ	653		653
Q	2101	ACACCTAGCGGAGCGATGCCCAACCAGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG	2160

VERSION AR080259.1 GI:10006994 KEYWORDS SOURCE UNKNOWN. ORGANISM UNKNOWN. Unclassified. REFERENCE 1 (bases 1 to 4473) AUTHORS Bennett, C. Frank, Lipton, A. and Witters, L.M. TITLE Antisense oligonucleotide modulation of human HER-2 expression JOURNAL Patent: US 5968448-A 1 19-CT-1999; FEATURES Location/Qualifiers SOURCE AOTHORS LOCATION/QUALIFIERS AOTHORS	Scores: 1.61e-229 Length: 4473 3776.00 Matches: 712 Similarity: 67.94% Conservative: 0 Similarity: 67.94% Mismatches: 0 h: 67.94% Mismatches: 0 h: 95.50% Indels: 336 6 Gaps: 1 2) x AR080259 (1-4473) 1 MetGluLeuAlaAlaLeuCySArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 1	175 ATGGGGGCTTGTGCCGCTGGGGGGCTCCTCGCCCTCTTGCCCCCGGGGGCC 234	81 GlnGlyTyrValLeurleAlaHisAsnGlnValArgGlnValProLeuGlnArgGluArgGlnValProLeuGlnArgGluArgGluNalProLeuGlnArgGluArgGluNalProLeuGlnArgGluArgGluNalProLeuGlnArgGluArgGluNalProLeuGlnArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGluArgGlu	161 LeuCysTyrGlnAspThrileLeuTrpLysAspIlePheHisLysAsnAsnCocococococococococococococococococococ
653 2161 653 2221 653 2281	Db 2341 TATGTCTCCGCCTTCTGGGCATCTGCCTGACATCCAGGTGCAGCTGGAGCACAGCTT 2400 Qy 653	QY 653	Qy 653	QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspAspAspAspAspAspAspAspAspAspAspA

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oy Ob	261 SerGlyIleCysGluLeuHiSCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280 	Q Q	621 GlyalaCysGlnProCysProIleasnCysThrHisSerCysValaspLeuaspAspLys 640
Oy Db	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	k qa	641 GlyCysProalaGluGlnArgalaSerProLeuThrSer
Qy	301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320 	y do	653 653 2155 ATTCTGCTGGTCGTCTTGGGGTCGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2214
O D	321 GluValThralaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340 	yy da	653 653 2215 AAGATCCGGAAGTGCGGAGAACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2274
Qy Dp	341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360 	ý a	653 653 2275 ACACCTAGCGGAGGGGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2334
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Qy Dp	81 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	Qy Db	653 653 2395 CCTGATGGGGAGAAATGTGAAAATTCCAGTGGCCATCAAAGTGTTGAGGGAAAACACATCC 2454
Qy Dp	401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420 	y d	653 653 2455 CCCAAAGCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGGCTCCCCA 2514
oy O	AspleuSerValPheGlnAsnLeuGlnVallleArgGlyArgllLeLeuHisAsnGlyAla 	Qy	3
Oy DD	441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460 	ç d	3
Oy Db	461 LeuGlySerGlyLeuAlaLeuIleHiSHiSASnThrHiSLeuCySPheValHiSThrVal 480 	ç da	GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG
Oy Db	481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500 	상 원 -	653 653 2695 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGAAGAGTCCCAAGCATGTCAAA 2754
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δο QΩ	521 TrpGlyProflyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 	da Dp	3
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Qy Dp	581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 	g g	2995 CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG 3054
oy.	1 ProSerGlyValLysProAspLeuSerTyrMetProlleTrpLysPheProAspGluGlu	γο	

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δλ	654	දු	
qa	3115 AGGACCCCCAGCGTTTGTGGTCATCCAGAATGAGGACTTGGGCCCAGCCAG	Qy St.	141 GlnLeuArgSerLeuThrGluI]
Qy Db	665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684	70 70	161 LeuCysTyrGlnAspThrIleLe
^O	GluGluTvrLeuValProGlnGlnGlvPhePheCvsProasnproAlabroGlvalvalv70	qa	655 CTCTGCTACCAGGACACGATTT
- q ₀		δλ	181 LeuThrLeuIleAspThrAsnA
Qy	705 GlyMetValHisHisArgHisArg 712	ଫୁପ %	715 CTCACACTGATAGACACCAACCC
	3295 GGCATGGTCCACCACAGGCACCGC 3318	ZZ qQ	201 GIYSELAIGCYSILPGIYGIGG
RESULT 10 AR167390		δŏ	
DEFINITION	AKLO/350 Weduence 26 from patent US 6287569. ARI67390	q _Q	835 GCCGGTGGCTGTGCCCCCCTGCA
VERSION		δλ	241 AlaAlaGlyCysThrGlyProLy
SOURCE	Unknown. Diknown.	ପ୍ପ	895 GCTGCCGGCTGCACGGCCCCAA
REFERENCE		δŏ	261 SerGlyIleCysGluLeuHisCy
AUTHORS	Kipps,T.J. and W.Y. Vaccines with onbanced intracellular proceeds	අ	955 AGTGGCATCTGTGAGCTGCACTC
JOURNAL	ט ט	Qy	281 SerMetProAsnProGluGlyAr
sonrce	:e 14473 //pressiem="unbessim"	qa	1015 TCCATGCCCAATCCCGAGGGCCC
BASE COUNT	/ / / / / / / / / / / / / / / / / / /	0y	301 TyrasnTyrLeuSerThraspVa
Alicatin A		q	1075 TACAACTACCTTTCTACGGACGI
Pred. No.:	1.61e-229 Length:	٥٧	321 GluvalThrAlaGluAspGlyTh
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_	caps.	qu	1195 GTGTGCTATGGTCTGGGCATGGA
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qa		qa	1375 GAGACTCTGGAAGAGATCACAGG
Qy	/rLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	δy	421 AspLeuSerValPheGlnAsnLe
qa		qq	1435 GACCTCAGCGTCTTCCAGAACCT
Oy	10	δλ	441 TyrSerLeuThrLeuGlnGlyLe
qq		qa	1495 TACTCGCTGACCCTGCAAGGCCT
^	101 IleValArqGlvThrGlnLeuPheGluAspAsnTvrAlaLeuAlaValTeuAspAsnGlv 120	QY	461 LeuGlySerGlyLeuAlaLeuIl
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Οÿ	121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140	δλ	481 ProTrpAspGlnLeuPheArgAs

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                       CCTGTCACAGGGGCCTCCCCAGGAGGCCTGCGGGGAGCTG
         SluHisLeuArgGluValArgAlaValThrSerAlaAsn
                                                                                                                                                    AsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe
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376. 384
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1885. 1893
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Halpern,M.S. and England,J.M.
Cellular immunogens comprising cogn.
Patent: US 6365151-A 4 02-APR-2002;
Location/Qualifiers
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67.948
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     Unclassified
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SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280 	SerMetBroAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 30	TyrasnTyrLeuSerThraspValGlySerCysThrLeuValCysProLeuHisasnGln 320	alaGluaspGlyThrGlnargCysGluLysCysSerLysProCysAlaarg 34. 	ValcysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 36 	IleGinGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuPrOGluSer 38	PheaspGlyaspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 40	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 42 	AspleuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 4. 	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 46 	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 48 	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 50 	GluAspGluCysValGlyGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520 	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540 	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560 	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580 	AlaAspGlnCysValAlacysAlaHisTyrLysAspProProPheCysValAlaArgCys 600 	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPhePro
261 S 931 A	281 S	01	321 G 1111 G	341 V 1171 G	361 I 1231 A	381 P	401 G 1351 G	421 A 1411 G	441 T 1471 T	461 I 1531 C	481 P	501 G 1651 G	521 T 1711 T	541 V 1771 G	561 L 1831 T	581 A	601 P 1951 C
Oy Dp	oy Op	Qy	Oy Dp	Qy	Oy Db	Oy Dp	Qy Db	Qy Dp	Oy Db	Qy Db	Qy	oy Op	Qy	Oy Dp	Qy Dp	oy D	Oy Dp

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LACHQLCARGHCWGPGPTQCVNCSQFLRGQECVEECRVLQGLPREYUNARHCLPCHPE CQCQPGNGSYTCTGCPECARGTAKDDPFCSARGNYBDLZXMPINKFDDEGACQ PCPINCTHSCVDLDDNGCPARGNASPLTSIVSAVVGTLLVVVLGSVAPFINKFRQXI RKTYMRRLLOGTELVPECTAPGGAMPNOAQMRILKEFELRKVVLGSGAFGTVYKGIWI PDGBNVKIPVARTYKULRENTSPKANKETLDEAYWAGVGSPYVSRLLGTCTTSYVQLVT QLMPYGCLLDHVRENNGRLGSQDLLNMCQIAKGMSYLEDVRLVHRDLAARNVLVKSP NHYKTTDFGLARLLDIDETBYHADGGKVPIKWAALESILRBRRTHQSDVWSYGVTVWE LWTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYMINVKCWMIDSECRPRFREL VSEFSERAARDPOSFRVYIQNEDLCAPSTFYRSLLEDDDWGDLVDAEETLVPQOGF FCPDPAPGAGGMVHHRHRSSSTRSGGDLTLLCLEPSEEEAPRSPLAFSEGAGSDVFDG DLGWGAAKGLQSLPHNDSPLOKYSEDPTVPLSETDGYVAPLTCSPQFEXUPOGGF FCPDPAPGAGGMVHHRHRSSSTRSGGDLTLCLEPSEEEAPRSPLAFSEGAGSDVFDG DLGWGAAKGLQSLPHNDSPLOKYSEDPTVPLSETDGYVAPLTCSPQFEXUPOGGF PQPHPPPAFSPARPAGATLERAKTLSPGGAVENPEYLGLDDVPV BASE COUNT 922 a 1382 c 1346 9 880 t 0RIGIN	res: 1.63e-229 Length: 3776.00 Matches: 712 3776.00 Matches: 712 4530 milarity: 67.94% Conservative: 0 milarity: 67.94% Mismatches: 0 55.50% Indels: 336 6aps: 1 AX282577 (1-4530) MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLroProGlyAla 20	151 ATGGAGCTGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	Qy 61 GluLeuThrTyrLeuProThrAsnalaSerLeuSerPheLeuGlnAspIleGlnGluVal 80 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
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Oy 2	241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260	Qy Dp	601 ProSerGlyValLy
	GVIGVCIGGCIGGCGCCCCCGGGGCCCITGGCIGGCCIGGC	Qy	621 GlyAlaCysGlnPr
	ი ი	Dp	2011 GGCGCATGCCAGC
	SerWet ProAsnProGluGlvArcTvrThrPheGlvAlaSerCvsValThralaCvsDro 30	QY	641 GlyCysProAlaGl
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1		qa	2131 ATTCTGCTGGTCGT
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	ValCvsTvrGlvLenGlvMetGluHisLenArgGluValArglaValmbrgeralaaen 360	Qy	653
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-	401 LeuciysefciyLeuAialeuileHishisAssiinrHisLeucysPheVaIHisThrVal 480 	qq	2611 GACCTGCTGAACTG
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                  AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla
                                           --GlnAsnGluAspLeuGlyProAlaSerProLeu
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370	AGGAAGGTGAAGGTGCTTGG	2311	g
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00	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCy	581	7
.80 890	. LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 5	561 1831	λ 2
		1771	g
09	ValGluGluCysArqValLeuGlnGlyLeuProArqGluTyrValAsnAlaArqHisCy	541	Š
40.770	. Trp6lyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 5 1111111111111111111111111111111111	521	8 3
710		1651	9
20	GluAspGluCysValGlyGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCy	501	Š
.650	ProTrpaspGlnLeuPheArgasnProHisGlnAlaLeuLeuHisThrAlaasnArgPro 5	481 1591	≳ 43
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530	TACTCGCTGACCCTGCAAGGCTTGGGCATCAGCTGGGCTTGGGCTTGCGCTCACTGAGGGA		e,
60	TyrSerLeuThrLeuGlnGlyLeuGlylleSerTrpLeuGlyLeuArgSerLeuArgGlu 	441	7 4

QQ	2551	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGGACGCCTGGGCTCCCAG 2	2610
Qy.	653	9	653
qq	2611	GACCTGCTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2	2670
Qy	653		653
qa	2671	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCCAACCA G	2730
Qy	653	9	653
qq	2731	ATTACAGACTTCGGGCTGGCTCGGCTGGTGGACATTGACGAGACAGAĞTACCATGCAGAT 2	2790
ΟY	653	9	653
qq	2791	GGGGGCAAGGTGCCCATCAAGTGGATGCGCTGGAGTCCATTCTCCGCCGGCGGTTCACC 2	2850
Qy	653		653
qq	2851	CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGGAGCTGATGACTTTTGGGGCCC 2	2910
Qy	653		653
Db	2911	AAACCTTACGATGGGATCCCAGCCCGGGAGATCCCTGACCTGCTGGAAAAGGGGGAGCGG 2	2970
ΟY	653		653
qq	2971	CTGCCCCAGCCCCCATCTGCACCATTGATGTCTACATGATCATGGTCAAATGTTGGATG	3030
Qy	653		653
Db	3031	ATTGACTCTGAATGTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCCGCATGGCC	3090
Qy	654	GlnAsnGluAspLeuGlyProAlaSePProLeu	664
qq	3091		3150
Qy	999		684
QQ	3151	GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGGACCTGGTGGATGCT	3210
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pp	3211		3270
Qy	705	GlyMetValHisHisArgHisArg 712	
Dþ	3271	GGCATGGTCCACCACGGCACGC 3294	
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 15, 2003, 22:47:19; Search time 7192.52 Seconds

(without alignments)
3105.423 Million cell updates/sec

Title: SEQ6

Perfect score: 5078
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Scoring table: BLOSUM62
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Ygapop 6.0, Fgapext 7.0
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Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784
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Minimum DB seq length: 0 Maximum DB seq length: 20000000000

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Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404N10 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived
ACCESSION
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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AL Nature 420, 563-573 (2002)

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SE Adachi, J. Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Haranco, R., Hiramoto, K., Hiranca, T., Hayashida, K., Hayashida, K., Enbili, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Mishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, V., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Shinaki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaru, A., Toya, T., Yasunishi, A.,
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail-genome-reségsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
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Qy 904 ThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919	AKOR ON Mus enri leur Oncc A AKOR	SOURCE Mus musculus (house mouse) ORGANISM Mus musculus ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. AUTHORS Carninci, P. and Hayashizaki, Y. TITLE High-efficiency full-length cDNA cloning JOGNNAL Meth. Enzymol. 303, 19-44 (1999) PUBMED 10349636	REFERENCE 2 AUTHORS 2 AUTHORS, Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazakı,Y., Muramatsu,M. and Hayashizakı,Y. TITLE Normalization and subtraction of cap-trapper-selected cDNAs to JOURNAL Genome Res. 10 (10), 1617-1630 (2000) MEDLINE 20499374 PUBMED 11042159 PREPERENCE	AUTHORS Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Ronno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yoneda, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiwafi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Squencing pipeline with 384 multicospillary sequencer Society and Society Soc		Carningle, P., de Hondado, M. F., Brownstein, M., is Bulf.C., Fletcher, C., Fujita, M., dearboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., TOYO-Oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. TITLE Functional annotation of a full-length mouse cDNA collection Neutre, 409 (6821), 685-690 (2001) MEDLINE 11217851 SREFERENCE 5 AUTHORS Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation
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/strain="c57BL/6J"
/db_xref="FANTOM_DB:D030063B12"
/db_xref="taxon:10090"
/clone="r0030063B12"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="9 days embryo"
/note="v-erb-b2 erythroblastic leukemia viral oncogene
homolog 2, neuro/glioblastoma derived oncogene homolog (avian) (MGD|MGI:95410, GB|U71126, evidence: BLASTN, 99%, match=449)"
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/organism="Mus musculus"
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of 60,770 full-length cDNA.
Nature 420, 563-573 (2002)
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qq	1968 ACGAGGCTGCCCAGCAGAGCAGAGCCAGCCAGTGACATTCATCATTGCAACTGTGGT 2027	qq	
οy	652 652	oy :	656 uAspLeuGlyProAlaSerProLeuA
QQ	2028 GGGCGTCCTGTTCCTGATCATAGTGGTGGTCATTGGAATCCTAATCAAACGAAGGCG 2087	QQ	00
δy	652 652	Ολ	676 pAspMetGlyAspLeuValAspAlaG
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οy	652 652	λo i	696 SProAspProAlaProGlyAlaGlyC
qq	2148 CGAGGGCCTCCTAGCACCCCCTTGGCTTTGCAGCTAGCTGGGCATTCACCCTACCACCCT 2207	QQ ·	20
Qy	652 652	Oy	716 rArgSerGlyGlyGlyAspLeuThrI
Db	2208 CTCGCTCCAGCTGGAGGCCGCTGACGCCCAGTGGAGCTGTGCCCAACCAGGCTCAGAT 2267	අධ	
δy	652 652	Oy.	736 gSerProLeuAlaProSerGluGlyP
QQ	2268 GCGGATCCTAAAGGAGACAGAGCTAAGGAAGCTGAAGGTGCTTGGGTCAGGAGCCTTCGG 2327	qq	8
Qy	652 652	Ολ	756 tGlyAlaAlaLysGlyLeuGlnSerI :
QQ	2328 CACTGICTACAAGGGCATCIGGAICCCAGAIGGGGAGAACGIGAAAAICCCCGIGGCCAI 2387	අු .	ω ,
Qy	652 652	Oy	776 rSerGluAspProThrValProLeuF
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2448	CGTCATGGCTGGTGTGGGTTCTCCATATGTGTCCCGCCTCCTGGGCATCTGCCTGACATC 2507
652	652
2508	CACAGTGCAGGTGACACACGTTATGCCCTATGGCTGCCTTCTGGACCATGTCCGAGA 2567
652	652
2568	ACACCGAGGTCGCTTAGGCTCCCAGGACCTGCTCAACTGGTGTTCAGATTGCCAAGGG 2627
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652	652
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2808	ATCTATICTCAGACGCCGGTICACCCAICAGAGTGATGTGTGGAGCTATGGTGTGACTGT 2867
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652	652
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2988	CATGATCATGGTCAAATGTTGGATGATTGACTCCGAATGTCGCCCGAGATTCCGGGAGTT 3047
653	56 Linini
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3108	GGACTTAGGCCCCTCCAGCCCCATGGACAGCACCTTCTACCGTTCACTGCTGGAGGATGA 3167
7	heCy 696
3168	igaagagracciggracccagcaggafic
696 3228	SProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSerSerSerTh 716
716	:lyGlyGlyAspLeuThrLeuGlyLeuGluProSerGluGluGluAlaProAr 73
3288	
736	gSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMe 756
*	#C166C1CCC1CC6AA6666C166C1CC6A161116A16616ACC166CA61 340
756 3408	tGlyalaalaLysGlyLeuGlnSerLeuProThrHisAspProSerProLeuGlnArgTy 776
3468	rSerGludspProThrValProLeuProSerGluThraspGlyTyrValAldProLeuTh 796

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                 Mus musculus 13 days embryo male testis CDNA, RIKEN full-length enriched library, clone:6030449F08 product:v-erb-b2 erythroblastic lenkemia viral oncogene homolog 2, neuro/glioblastoma derived AK031542. I GI:26327396
                                                                                                             1588 CCCAGAGGGTCCTCCGCCTCCCATCCGACCTGCTGCTACTCTAGAAAGACCCAAGAC 3647
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                                                                                                                                                     856
                                                                                                                                                                                                                              uAsnProGluTyrLeuThrProGlnGlyGlyAlaAlaAlaProGlnProHisProProProAl 876
rCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnProProSerPr 816
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                         816 oArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaThrLeuGluArgProLysTh
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                                                                                             Carninci, P. and Hayashizaki, Y.
Igh-effictency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuell,P., Lewis,S., Matsuo,Y., Nikatdo,I., Pesole,G., Ouackenbush,J., Schriml,L.M., Staubil,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., Ge Bonaldo,M.F., Brownstein,M.J., Bult,C., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Hill,D., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Nature 420, 563-573 (2002)

E (bases 1 to 3110)

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verb-b2 erythroblastic leukemia viral oncogene homolog 2,
neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MGI:95410, GB|U71126, evidence: BLASIN, 99%,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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GPPPSTFEGTPARRHPETLARRAGTASQPHPSPAFSPAFDNLYYWDGNSSEQ
GPPPSTFEGTPARRHPETLARRAGTASQPHPSPAFSPAFDNLYYWDGNSSEQ
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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_	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning L Meth. Enzymol. 303, 19-44 (1999) E 99279253 P 10349636				Fulwake, S., Indue, K., Togawa, Y., Izawa, M., Onara, E., Wateniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Riken integrated sequence analysis (RISA) system384-format		S Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakewa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,	SalCorr., OrderArtir, Goldborr., Bono, Hr., Assukawarr., Sallo, R., Kaddta, Y., Matsuda, H., Ashburner. M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,	Quackenbush,J., Schill,L.M., StabbliF., Suzuki,K., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bolunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,	Fletcher,C., Fujita,M., Gariboldi,M., Gustinoich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.	Functional annotation of a full-length mouse cDNA collection L Nature 409 (6821), 685-690 (2001) E 21085660 D 11217851			Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itch, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
VERSION KEYWORDS SOURCE ORGANISM REFERENCE	AUTHORS TITLE JOURNAL MEDLINE PUBMED	AUTHORS	MEDLINE PUBMED REFERENCE	AUTHORS	TITLE	JOURNAL MEDLINE PUBMED	AUTHORS				\$ 8 8	TITEE JOURNAL MEDLINE PUBMED	AUTHORS TITLE	JOURNAL REFERENCE AUTHORS	
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                                                                                                                                                                      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' schools of the second was prepared with the primer adapter of sequence[5' schools of the second was the second with NoI and StI. Cloning sites, 5' end: SSII; 3' end: NoI. Host: SOLR.
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                                              Yoshida, K.
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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                                                                                     ThrAspMetLysLeuArgLeuProAlaSerProGluThrHisLeuAspMetLeuArgHis
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                                                                                                                         AlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTyrValLeuIleAlaHis
                                                                                                                                                 475 TACGACCTTTCCTTTAAAGACCATCCAGGAGGTGGCCGGCTATGTCCTCATTGCCCTC
                                                                                                                                                                          AsnGlnValArgGlnValProLeuGlnArgLeuArgIleValArgGlyThrGlnLeuPhe
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                   GATTCTTTCACGCGCACTCCTCTTAGACCCACGAGAACTAGAAATTCTAAAAACCGTA 1449
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                     AspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPheGluThrLeu 403
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Physical and Chemical Research (RIKEN), Laboratory for Genome Payloration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:Genome-reseggsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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/db_xref="hMI:1896853"
/db_xref="taxon:10090"
/clone="130003K07"
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             AsnGlnValArgGlnValProLeuGlnArgLeuArgIleValArgGlyThrGlnLeuPhe
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                                                AlaSerLeuSerPheLeuGlnAspilleGlnGluValGlnGlyTyrValLeuIleAlaHis
                                                                                                           ---TATGGGACAAACAGAACTGGGCTTAGGGAACTGCCCATGCGGAACTTACAGGAAATC
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EDHFLSLQRAYNNCEVVLGNLEITYVCRNYDLSFLKTIGEVAGY VLIALNYVERIPLE
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                                                                     AlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTyrValLeuIleAlaHis
                                                                                       TACGACCTTTCCTTCTTAAAGACCATCCAGGAGGTGGCCGGCTATGTCCTCATTGCCCTC
                                                                                                                                          AsnGlnValArgGlnValProLeuGlnArgLeuArgIleValArgGlyThrGlnLeuPhe
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LeuTyrGlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThrTyrLeuProThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLysGlySerArgCys
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NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1709 AAACTCTTCGGGACACCCCAATCAGAAAACCAAAAATCATGAACAACAAGAGAAGAC
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                                                                                                                                                                                                              CysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCysLeuProCys
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                              ValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAlaTyrSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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/lab_host="adult, 36 yr"
/lab_host="bHl0B"
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Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gow.f column: 06

High quality sequence start: 27

High quality sequence stap: 529.

Location/Qualifiers

I. 964

/organism="Homo sapiens"
//db_xref="mkan":966"
//db_xref="mkan":9666"
//clone="IMAGE:6180101"
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Gaps:
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/codon_start=1
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/protein_id="AAL55856.1"
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/translation="MALESILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIPAREIP
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Hunday, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao, X.T., Wan, D.F. and Gu, J.R.
Novel human cDNA clones with function of inhibiting cancer cell
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                                                                                                                           yHisCysTrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGl
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Huang,Y., Zhou,X.M., Zhang,P.P., Jiang,H.Q.,
Wan,D.F. and Gu,J.R.
Waret Submission
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Homo sapiens pp3659 mRNA, complete cds.
AF318349
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/cloned with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
a 297 c 261 g 149 t
                                   885 bp mRNA linear EST 12-NOV-2002
Homo sapiens cDNA clone IMAGE:6722585 5',
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/mol_type="mRNA"
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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
                                                                                     888
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs.remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI485 row: i column: 17
High quality sequence stop: 717.
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Contact: Robert Strausberg, Ph.D.
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/lab_host="EMDH10B"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.
                                        ProLeuThrCysSerProGlnProGluTyrValAsnGlnProAspValArgProGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                            GluAspAspAspAetGlyAspLeuValAspAlaGluGluTyrLeuValProGlnGlnGly
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Mus musculus, clone IMAGE:5340777, mRNA.
BC046553
BC046553.1 GI:28196923
HTC.
 Gaps:
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                    (1-919) x CA455074 (1-885)
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TITLE Direct Submission JOURNAL Submitted (03-FEB-2003)	National Institutes of Health, Mammalian	Óλ	652 652
Gene Collection (MGC), Institute, 31 Center Dr	Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	qa	596 ATGCGTAGGCTGCTGCAGGAGCGGAGCTGGAGCCGCTGACGCCCCAGTGGAGCTGTG 655
USA REMARK NIH-MGC Broject HRI: bt	to.//mac not nih acu	Qy	652 652
	Contact: MGC help despired in the MGC help d	qa	656 CCCAACCAGGCTCAGATGCGGATCCTAAAGGAGGAGGCTAAGGAAGCTGAAGGTGCTT 715
Tissue Procurement: Lot	thigh Henrighausen Ph.D., Chu-Xia Deng Ph.D.	Qy	652 652
CDNA LIBRARY Arrayed by DNA CACHOROLIA HIS	7: The I.W.A.G.E. Consortium (LLNL)	qq	716 GGGTCAGGAGCCTTCGGCACTGTCTACAAGGGCATCTGGATCCCAGATGGGGAAACGTG 775
Sequencing by: bayi	tor correge or medicine Human Genome	Qy	652 652
Web site: http://www.hg	gsc.bcm.tmc.edu/cdna/	QQ	776 AAAATCCCCGTGGCCATCAAGGTGTTGAGGGAAAACACATCTCCTAAAGCTAACAAAAA 835
Gunaratne, P.H., Garcia	Contact: amgebom.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,	Qy	652 652
A.N., Gibbs, R.A.	J., Mailli, K.G., Muzny, D.M., Nanavali,	qq	836 ATCCTAGATGAAGCGTACGTCATGGCTGTGGGGTTCTCCATATGTGTCCCGCCTCCTG 895
Clone distribution: MGC	Clone distribution: MGC clone distribution information can be found	Qy	652 652
CHICUSH CHE 1.M.A.C.E. Series: IRAK Plate: 92 This clone has the foll	chlodgh the liming. Cousolttum/Limin at: http://limage.limi.gov Series: IRAK Plate: 92 Row: n Column: 17 This clone has the following problem: no K' nor match	qa	896 GGCATCTGCCTGACATCCACAGTGCAGCTGGTGACACAGCTTATGCCCTATGCCTTT 955
FEATURES Location/Quali	Ifiers	Qy	652 652
io/	s musculus"	qa	956 CTGGACCATGTCCGAGAACACCGAGGTCGCTTAGGCTCCCAGGACCTGCTCAACTGGTGT 1015
/*************************************	/strain=1129/2DL/6J.FVB/N" /strain=1129/2DL/6J.FVB/N"	Qy	652 652
/dD_Aifer - CaAC /Clone="IMAGE: /+iceus tunger	15.140090 15340777	qa	1016 GTTCAGATTGCCAAGGGGATGAGCTACCTGGAGGAAGTTCGGCTTGTTCACAGGGACCTA 1075
months old, gr	illouer.	Qy	652 652
/crone_iib / /lab_host="bhi /notes="vector"	LOST CONTROL C	qa	1076 GCTGCCCGAAACGTGCTAGTCAAGAGTCCCAACCACGTCAAGATTACCGACTTCGGGCTG 1135
BASE COUNT 754 a 944 c 9	926 g 748	Οy	652 652
Alignment Scores:		qq	1136 GCACGGCTGCTGGACATTGATGAGACTGAATACCATGCAGATGGGGGGCAAGGTGCCCATC 1195
	Length: 3372	Qy	652 652
Percent Similarity: 44.418 Best Local Similarity: 42.248	ative: hes:	qa	1196 AAGIGGAIGGCATIGGAATCIATICICAGACGCCGGITCACCCAICAGAGIGAIGIGG 1255
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26 (1-919) x BC046553		qa	1256 AGCTATGGTGTGTGTGGGAGCTGATGACCTTTGGGGCCAAACCTTACGATGGATC 1315
Ov 567 CvsGlnProGlnAenglvSer	Valmbrovebbeglvbroglualaben()morestalala 596	Oy	652 652
251		QQ	1316 CCAGCTCGGGAGATCCCTGATTTGCTGGAGAAGGGAGAACGCCTACCTCAGCCTCCAATC 1375
		Qy	652 652
296	TGTGCCCACTACAAGGACTCATCCTGTGTGTGGCTCGCTGCCCAGTGGTGAAGCCA 355	qa	1376 TGCACCATCGACGTCTACATGATGATGTTGGATGATGATTGACTCCGAATGTCGC 1435
Qy 607 AspLeuSerTyrMetProlle		Οy	652 652
Db 356 GACCTCTCCTACATGCCTATC	IIIÎ! CATGC	qa	CCGAGATTCCGGGGAGTTGGTATCAGAATTCTCCCGTATGGCAAGGGACCCCCAGCGCTTT
Qy 627 ProlleAsnCysThrHisSer	ProlleAsnCysThrHisSerCysValAspLeuAspAspLysGlyCysProAlaGluGln 646	oy 4	SerGlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPheTyrArg
Db 416 CCCATCAACTGCACCCACTCC	CCCATCAACTGCACCCACTCCTGTGTGGACCTGGACGAGGAGGCTGCCCAGCAGAGGAGG 475	3 8	#1 #61 CA1 CCA1 #4 #4 #4 #4 #4 #4 #4 #4 #4 #4 #4 #4 #4
Oy 647 ArgAlaSerProLeuThr		d d	0/1 Settedledutaspaspaspastoristic 090 1
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		qa	1616 CAGCAGGGATTCTTCTCCCCAGACCCTGCCTAGGTACTGGGAGCACAGCCCAGCGCAGA 1675
	CCITATION CONTROCCON CONTROLL COCCURACION CONTROLL CONTRO	Qy	711 HisArgSerSerThrArgSerGlyGlyGlyAspLeuThrLeuGlyLeuGluProSer 730

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314 ValCysProLeuHisAsnGlnGluValThrAlaGluAspGlyThr-GlnArgCysGlu-L 333
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94.66%
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Best Local Similarity:
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mRNA linear EST 20-FEB-2002 sapiens CDNA clone IMAGE:5736771
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                   LeuGluArgProLysThrLeuSerProGlyLysAsnGlyValValLysAspValPheAla
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                           GluGluGluAlaProArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapDs-remail.nh.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
found distribution: MGC clone distribution information on found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12745 row: n column: 04
High quality sequence stop: 637.
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HOMO
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Contact: Robert Strausberg, Ph.D.
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AGENCOURT_6566679 NIH_MGC_88
5', mRNA sequence.
BM562913
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Homo sapiens
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TITLE
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/db_xref="taxon:9606"
/clone="InAGE:5736771"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_l: Notl, Site_l: Sali; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
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Matches:
Conservative:
Mismatches:
Indels:
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à	VSCVsSpr[vsproCvsA]aArdVa]CvsTvrg]v[a]vWotG]iHislan	qa	187 TTCTTCT
	AGTGCAACCAGCCCTGTGCCCCCAGATGGGCTAATGGGCCTGGGGGTTGGAACATT	ý á	714 SerSerT
RESULT 12 CA455141 LOCUS DEFINITION	CA455141 AGENCOURT_10735980 MAPCL Homo sapiens cDNA clone IMAGE:6722663 5',		
ACCESSION VERSION KEYWORDS	mkna sequence. CA455141 CA455141.1 GI:24905561 EST.	Qy	754 LeuGlyMe 367 CTGGGAA
SOURCE ORGANISM	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AQ QQ	774 GlnArgTy 427 CAGCGGTA
REFERENCE AUTHORS TITLE JOURNAL	1 (Dases 1 to 893) NIH-MGC http://mgc.ncl.nih.gov/. NIH-MGC http://mgc.ncl.nih.gov/. National institutes of Health, Mammalian Gene Collection (MGC) Unpublished		
	Email: cgabbs-remail.nih.gv Tissue Procurement: Kristi A. Egland, Ira Pastan CDNA Library Preparation: Invitrogen Corp	Qy	814 ProSerP1 547 CCTTCGCC
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	Qy	
FEATURES	nccp://im Plate: LL High qual	oy Oy	854 AlavalG] 667 GCCGTGG
Sonos		Qy	874 ProProA]
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BASE COUNT ORIGIN	Manuscript submitted." 175 a 302 c 261 g 155 t	DEFINITION	AU140362 E sequence. AU140362
Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB:	Alignment Scores: 4.43e-83 Length: 893 Pred. No.: 1399.50 Matches: 261 Score: 1399.50 Matches: 261 Score: 298.13 Conservative: 1 Best Local Similarity: 97.75\$ Mismatches: 3 Query Match: 27.56\$ Indels: 2 DB: 14 Gaps:	VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	AU140362.1 EST. Homo sapic Homo sapic Eukaryota; Mammalia; 1 (bases Ota,T., Su
SEQ6 (1-919)	9) x CA455141 (1-893)	TITLE	Nishikawa, HRI human Yamamoto.
		JOURNAL	Masuho,Y., Unpublishe Contact: 1 Genomics I
oy da	674 GludspaspaspaspatelyaspieuValaspalaGluGluTyrLeuValProGlnGlnGlnG 693 		Helix Rese 1532-3 Yar Tel: 81-43 Fax: 81-43

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757 bp mRNA linear EST 05-AUG-2002 PLACE2 Homo sapiens cDNA clone PLACE2000402 5', mRNA
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; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Suzuki,Y., Salto,K., Ishii,S., Yamamoto,J., Sugiyama,T.,
Suzuki,Y., Makamura,Y., Sugano,S., Masuho,Y. and Isogai,T.
in cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S.,
y,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,
, Isogai,T.)
                                           ArgSerProLeuAlaProSerGluGlyAlaGlySerAspValPheAspGlyAsp
                                                                                                      ?ysProAspProAlaProGlyAlaGlyGlyMetValHisHisArgHisArgSer
           ThrLeuSerProGlyLysAsnGlyValValLysAspValPheAlaPheGlyGly
                                                                                                                                                                                                                                                                                                                                  Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
151-1 81-438-52-3975
Fax: 81-438-52-3986
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Email: genomics@hri.co.jp'
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

'S Location/Qualifiers

'I 757

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Mational Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-refmail.nh: gov

Tissue Procurement: Kristia A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be clone distribution; MGC clone distribution; MGC clone distribution: MGC clone distribution: LAM.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Location/Qualifiers

I. .894

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Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
                                                                                                                                                                                       CA*34131 894 bp mRNA linear EST 12-NOV-2002 AGENCOURT_10738550 MAPCL Homo sapiens CDNA clone IMAGE:6718792 5', MRNA sequence.
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663 AGGGAGTATGTGAATGCCAGGCACTGTTTGCCGTGCCACCCTGAGTGTCAGCCCCAGAAT 722
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	QQ	Qy Db	Qy	Qy	Qy Db	Qy	Qy Db	Qy	Qy B	0y ¹	QQ :	op Op	Qy Db	RESULT 15 CD515356 LOCUS	DEFINITION	VERSION KEYWORDS	SOURCE	REFERENC	AUTHORS	COMMENT				

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Location/Qualifiers
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Sequence 32, Appli
Sequence 34, Appli
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Sequence 11, Appli
Sequence 119, Appli
Sequence 119, Appli
Sequence 124, Appli
Sequence 125, Appli
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Sequence 17, Appli
Sequence 11, Appli
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Sequence 10, Appl
Sequence 24, Appl
Sequence 15, Appl
Sequence 11, Appl
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US-08-940-101-1
US-10-207-655-46
US-10-378-393-10
US-09-330-125-6
US-09-930-125-4
US-09-930-125-4
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APPLICANT: Corlax Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
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PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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16: /cgn2_6/ptodata/2/pubpna/USOB_BUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seg:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seg:*
               5.1.6
Compugen Ltd.
                                                                         nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                       of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             1750203 seqs, 1313063994 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3768 10 US-09-854-356-9
                GenCore version
Copyright (c) 1993 - 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB
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seq6.rnpb

LOCATION: (1)(3768) OTHER INFORMATION: human HER-2/neu protein NAME/KEY: misc_feature LOCATION: (1)(1959) OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu NAME/KEY: misc_feature LOCATION: (2065)(3765) OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu NAME/KEY: misc_feature LOCATION: (2968)(3765) OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu NAME/KEY: misc_feature LOCATION: (2968)(3144) OTHER INFORMATION: preferred portion of the phosphorylation domain OTHER INFORMATION: (delta PD) of human HER-2/neu	0 4900.00 73.23% : 73.23% 10 10	1 A US 09-834-336 9 (1.3/88) 1 MetGluLeualaalaLeuCysArgTrpGlyLeuLeuLeualaLeuLeuProProGlyala 20	21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40 	41 ThrHisLeuaspMetLeuargHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60 	61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80 	81 GlnGlyTyrValLeullealaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100 	101 IleValArgGlyThrGlnLeuPheGluAspAsnTyralaLeuAlaValLeuAspAsnGly 120 	121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140 		161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180 	181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200	001 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220	221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
LOCATION: OTHER INFE UCATION: OTHER INFE	nment No.: e: ent Si Local	1		ਜ	1	2	101	121	141	161	181	201	22
	Present of the presen	3	Qy Dp	Qy Dp	QY DP	Qy	QQ QQ	Qy	Q D	Qy Dp	QQ QD	δ qα	δλ

1080 1140 1260 1020 1200 1380 1440 1560 1320 1500 1620 1680 280 840 300 1800 260 780 320 340 360 380 400 420 440 900 960 460 480 540 720 500 520 560 580 009 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCCAGCTGTGTGACTGCCTGTCCC TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPhéGlyProGlu 1681 TTGCCGTGCCACCTGAGTGTCAGCCCCAGAATGGCTCAGTGACCTGTTTTGGACCGGAG TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 1021 1801 1141 401 1201 441 461 1381 481 1441 1501 1561 661 241 721 261 781 301 901 321 196 341 361 381 1621 281 501 521 541 561 581 Qγ g Qγ Ω δ g οy Ω ŏ g οy Q ò g ò qq à Db Q g δy 셤 qq q δ οy δy qq ò 엄 οq g qq ò δ